

SEQUENCE LISTING

<110> Reed, John C.  
Pio, Frederick F.  
Godzik, Adam  
Stehlik, Christian  
Damiano, Jason S.  
Lee, Sug-Hyung  
Oliveira, Vasco A.  
Hayashi, Hideki  
Pawlowski, Krzysztof

<120> Card3X-2 Polypeptides, Encoding Nucleic  
Acids, and Methods of Use

<130> 66821-267

<150> US 09/579,240  
<151> 2000-05-24

<150> US 09/686,347  
<151> 2000-10-10

<150> US 60/275,980  
<151> 2001-03-14

<150> US 09/864,921  
<151> 2001-05-23

<160> 203

<170> FastSEQ for Windows Version 4.0

<210> 1

<400> 1  
000

<210> 2

<400> 2  
000

<210> 3

<400> 3  
000

<210> 4

<400> 4

000

<210> 5

<400> 5

000

<210> 6

<400> 6

000

<210> 7

<400> 7

000

<210> 8

<400> 8

000

<210> 9

<400> 9

000

<210> 10

<400> 10

000

<210> 11

<211> 1038

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)...(930)

<400> 11

atg	gct	acc	gag	agt	act	ccc	tca	gag	atc	ata	gaa	aga	gaa	aga	aaa	48
Met	Ala	Thr	Glu	Ser	Thr	Pro	Ser	Glu	Ile	Ile	Glu	Arg	Glu	Arg	Lys	
1				5					10					15		

aag	ttg	ctt	gaa	atc	ctt	caa	cat	gat	cct	gat	tct	atc	tta	gac	acg	96
Lys	Leu	Leu	Glu	Ile	Leu	Gln	His	Asp	Pro	Asp	Ser	Ile	Leu	Asp	Thr	
			20					25					30			

tta	act	tct	cgg	agg	ctg	att	tct	gag	gaa	gag	tat	gag	act	ctg	gag	144
Leu	Thr	Ser	Arg	Arg	Leu	Ile	Ser	Glu	Glu	Glu	Tyr	Glu	Thr	Leu	Glu	
			35				40					45				

aat gtt aca gat ctc ctg aag aaa agt cgg aag ctg tta att ttg gta	192
Asn Val Thr Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val	
50 55 60	
cag aaa aag gga gag gcg acc tgt cag cat ttt ctc aag tgt tta ttt	240
Gln Lys Lys Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys Leu Phe	
65 70 75 80	
agt act ttt cca cag tca gct gcc att tgc ggc tta agg cat gaa gtt	288
Ser Thr Phe Pro Gln Ser Ala Ala Ile Cys Gly Leu Arg His Glu Val	
85 90 95	
tta aaa cat gag aat aca gta cct cct caa tct atg ggg gca agc agt	336
Leu Lys His Glu Asn Thr Val Pro Pro Gln Ser Met Gly Ala Ser Ser	
100 105 110	
aat tca gaa gat gct ttt tct cct gga ata aaa cag cct gaa gcc cct	384
Asn Ser Glu Asp Ala Phe Ser Pro Gly Ile Lys Gln Pro Glu Ala Pro	
115 120 125	
gag atc aca gtg ttc ttc agt gag aag gaa cac ttg gat ttg gaa acc	432
Glu Ile Thr Val Phe Phe Ser Glu Lys Glu His Leu Asp Leu Glu Thr	
130 135 140	
tct gag ttt ttc agg gac aag aaa act agt tat agg gaa aca gct ttg	480
Ser Glu Phe Phe Arg Asp Lys Lys Thr Ser Tyr Arg Glu Thr Ala Leu	
145 150 155 160	
tct gcc agg aag aat gag aag gaa tat gac aca cca gaa gtc aca tta	528
Ser Ala Arg Lys Asn Glu Lys Glu Tyr Asp Thr Pro Glu Val Thr Leu	
165 170 175	
tca tat tca gtt gag aaa gtt gga tgt gaa gtt cca gca act att aca	576
Ser Tyr Ser Val Glu Lys Val Gly Cys Glu Val Pro Ala Thr Ile Thr	
180 185 190	
tat ata aaa gat gga cag aga tat gag gag cta gat gat tct tta tac	624
Tyr Ile Lys Asp Gly Gln Arg Tyr Glu Glu Leu Asp Asp Ser Leu Tyr	
195 200 205	
tta gga aaa gag gaa tat cta gga tct gtt gac acc cct gaa gat gca	672
Leu Gly Lys Glu Glu Tyr Leu Gly Ser Val Asp Thr Pro Glu Asp Ala	
210 215 220	
gaa gcc act gtg gaa gag gag gtt tat gat gac cca gag cac gtt gga	720
Glu Ala Thr Val Glu Glu Glu Val Tyr Asp Asp Pro Glu His Val Gly	
225 230 235 240	
tat gat ggt gaa gag gac ttc gag aat tca gaa acc aca gag ttc tct	768
Tyr Asp Gly Glu Glu Asp Phe Glu Asn Ser Glu Thr Thr Glu Phe Ser	
245 250 255	

ggt gaa gaa cca agt tat gag gga tca gaa acc agc ctt tca ttg gag 816  
Gly Glu Glu Pro Ser Tyr Glu Gly Ser Glu Thr Ser Leu Ser Leu Glu  
260 265 270

gag gaa cag gag aaa agt ata gaa ggc tgg tct cga act cat ggg ctt 864  
Glu Glu Gln Glu Lys Ser Ile Glu Gly Trp Ser Arg Thr His Gly Leu  
275 280 285

aag cga tcc tcc cac gtt ggc ctc cca aag tgc tgg gat tac agg cgt 912  
Lys Arg Ser Ser His Val Gly Leu Pro Lys Cys Trp Asp Tyr Arg Arg  
290 295 300

gag cca ccc tgc ctg gcc tgaaaattct gcctcaaaca tctcaaacat 960  
Glu Pro Pro Cys Leu Ala  
305 310

ccatttatat tttgtacaag aaagtaaata aaatttttct ttttaacatt aaaaaaaaaa 1020  
aaaaaaaaaa aatctaga 1038

<210> 12  
<211> 310  
<212> PRT  
<213> Homo sapien

<400> 12  
Met Ala Thr Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys  
1 5 10 15  
Lys Leu Leu Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr  
20 25 30  
Leu Thr Ser Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu  
35 40 45  
Asn Val Thr Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val  
50 55 60  
Gln Lys Lys Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys Leu Phe  
65 70 75 80  
Ser Thr Phe Pro Gln Ser Ala Ala Ile Cys Gly Leu Arg His Glu Val  
85 90 95  
Leu Lys His Glu Asn Thr Val Pro Pro Gln Ser Met Gly Ala Ser Ser  
100 105 110  
Asn Ser Glu Asp Ala Phe Ser Pro Gly Ile Lys Gln Pro Glu Ala Pro  
115 120 125  
Glu Ile Thr Val Phe Phe Ser Glu Lys Glu His Leu Asp Leu Glu Thr  
130 135 140  
Ser Glu Phe Phe Arg Asp Lys Lys Thr Ser Tyr Arg Glu Thr Ala Leu  
145 150 155 160  
Ser Ala Arg Lys Asn Glu Lys Glu Tyr Asp Thr Pro Glu Val Thr Leu  
165 170 175  
Ser Tyr Ser Val Glu Lys Val Gly Cys Glu Val Pro Ala Thr Ile Thr  
180 185 190  
Tyr Ile Lys Asp Gly Gln Arg Tyr Glu Glu Leu Asp Asp Ser Leu Tyr  
195 200 205  
Leu Gly Lys Glu Glu Tyr Leu Gly Ser Val Asp Thr Pro Glu Asp Ala  
210 215 220

Glu	Ala	Thr	Val	Glu	Glu	Glu	Val	Tyr	Asp	Asp	Pro	Glu	His	Val	Gly
225					230				235						240
Tyr	Asp	Gly	Glu	Glu	Asp	Phe	Glu	Asn	Ser	Glu	Thr	Thr	Glu	Phe	Ser
				245					250					255	
Gly	Glu	Glu	Pro	Ser	Tyr	Glu	Gly	Ser	Glu	Thr	Ser	Leu	Ser	Leu	Glu
			260					265					270		
Glu	Glu	Gln	Glu	Lys	Ser	Ile	Glu	Gly	Trp	Ser	Arg	Thr	His	Gly	Leu
		275					280				285				
Lys	Arg	Ser	Ser	His	Val	Gly	Leu	Pro	Lys	Cys	Trp	Asp	Tyr	Arg	Arg
	290					295					300				
Glu	Pro	Pro	Cys	Leu	Ala										
305					310										

<210> 13

<400> 13  
000

<210> 14

<400> 14  
000

<210> 15

<400> 15  
000

<210> 16

<400> 16  
000

<210> 17

<400> 17  
000

<210> 18

<400> 18  
000

<210> 19

<400> 19  
000

<210> 20

<400> 20  
000

<210> 21

<400> 21  
000

<210> 22

<400> 22  
000

<210> 23

<400> 23  
000

<210> 24

<400> 24  
000

<210> 25

<400> 25  
000

<210> 26

<400> 26  
000

<210> 27

<400> 27  
000

<210> 28

<400> 28  
000

<210> 29

<400> 29  
000

<210> 30

<400> 30  
000

<210> 31

<400> 31  
000

<210> 32

<400> 32  
000

<210> 33

<400> 33  
000

<210> 34

<400> 34  
000

<210> 35

<400> 35  
000

<210> 36

<400> 36  
000

<210> 37

<400> 37  
000

<210> 38

<400> 38  
000

<210> 39

<400> 39  
000

<210> 40

<400> 40  
000

<210> 41

<400> 41  
000

<210> 42

<400> 42  
000

<210> 43

<400> 43  
000

<210> 44

<400> 44  
000

<210> 45

<400> 45  
000

<210> 46

<400> 46  
000

<210> 47

<400> 47  
000

<210> 48

<400> 48  
000

<210> 49

<400> 49  
000

<210> 50

<400> 50  
000

<210> 51

<400> 51  
000

<210> 52

<400> 52



000

<210> 53

<400> 53  
000

<210> 54

<400> 54  
000

<210> 55

<400> 55  
000

<210> 56

<400> 56  
000

<210> 57

<400> 57  
000

<210> 58

<400> 58  
000

<210> 59

<400> 59  
000

<210> 60

<400> 60  
000

<210> 61

<400> 61  
000

<210> 62

<400> 62  
000

<210> 63

<400> 63  
000

<210> 64

<400> 64  
000

<210> 65

<400> 65  
000

<210> 66

<400> 66  
000

<210> 67

<400> 67  
000

<210> 68

<400> 68  
000

<210> 69

<400> 69  
000

<210> 70

<400> 70  
000

<210> 71

<400> 71  
000

<210> 72

<400> 72  
000

<210> 73

<400> 73  
000

<210> 74  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 74  
tacttacttt gtcccttca 19

<210> 75  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 75  
tatttggtccc catctcgtc 19

<210> 76  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 76  
cggaattcat ggctaccgag agtactcc 28

<210> 77  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 77  
gtaaaacgac ggccagt 17

<210> 78  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 78  
gcagaagcca ctgtggaaga ggagggtt 27

<210> 79  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 79  
atacgactca ctatagggcg aattggcc 28

<210> 80

<220>  
<223> Primer

<400> 80  
000

<210> 81

<220>  
<223> Primer

<400> 81  
000

<210> 82  
<211> 3030  
<212> DNA  
<213> Homo sapien

<220>  
<221> CDS  
<222> (1)...(1680)

<400> 82  
tgt gaa atg tgc tcg cag gag gct ttt cag gca cag agg agc cag ctg 48  
Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu  
1 5 10 15

gtc gag ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg 96  
Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu  
20 25 30

gac tgg ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc 144  
Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly  
35 40 45

ttc cac ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg 192

Phe	His	Leu	Leu	Gly	Gln	Pro	Leu	Ser	His	Leu	Ala	Arg	Arg	Leu	Leu		
50						55					60						
gac	acc	gtc	tgg	aat	aag	ggt	act	tgg	gcc	tgt	cag	aag	ctc	atc	gcg	240	
Asp	Thr	Val	Trp	Asn	Lys	Gly	Thr	Trp	Ala	Cys	Gln	Lys	Leu	Ile	Ala		
65					70				75					80			
gct	gcc	caa	gaa	gcc	cag	gcc	gac	agc	cag	tcc	ccc	aag	ctg	cat	ggc	288	
Ala	Ala	Gln	Glu	Ala	Gln	Ala	Asp	Ser	Gln	Ser	Pro	Lys	Leu	His	Gly		
				85				90						95			
tgc	tgg	gac	ccc	cac	tcg	ctc	cac	cca	gcc	cga	gac	ctg	cag	agt	cac	336	
Cys	Trp	Asp	Pro	His	Ser	Leu	His	Pro	Ala	Arg	Asp	Leu	Gln	Ser	His		
			100					105						110			
cgg	cca	gcc	att	gtc	agg	agg	ctc	cac	agc	cat	gtg	gag	aac	atg	ctg	384	
Arg	Pro	Ala	Ile	Val	Arg	Arg	Leu	His	Ser	His	Val	Glu	Asn	Met	Leu		
			115				120							125			
gac	ctg	gca	tgg	gag	cgg	ggt	ttc	gtc	agc	cag	tat	gaa	tgt	gat	gaa	432	
Asp	Leu	Ala	Trp	Glu	Arg	Gly	Phe	Val	Ser	Gln	Tyr	Glu	Cys	Asp	Glu		
			130			135					140						
atc	agg	ttg	ccg	atc	ttc	aca	ccg	tcc	cag	agg	gca	aga	agg	ctg	ctt	480	
Ile	Arg	Leu	Pro	Ile	Phe	Thr	Pro	Ser	Gln	Arg	Ala	Arg	Arg	Leu	Leu		
145					150				155						160		
gat	ctt	gcc	acg	gtg	aaa	gcg	aat	gga	ttg	gct	gcc	ttc	ctt	cta	caa	528	
Asp	Leu	Ala	Thr	Val	Lys	Ala	Asn	Gly	Leu	Ala	Ala	Phe	Leu	Leu	Gln		
				165				170						175			
cat	gtt	cag	gaa	tta	cca	gtc	cca	ttg	gcc	ctg	cct	ttg	gaa	gct	gcc	576	
His	Val	Gln	Glu	Leu	Pro	Val	Pro	Leu	Ala	Leu	Pro	Leu	Glu	Ala	Ala		
				180				185						190			
aca	tgc	aag	aag	tat	atg	gcc	aag	ctg	agg	acc	acg	gtg	tct	gct	cag	624	
Thr	Cys	Lys	Lys	Tyr	Met	Ala	Lys	Leu	Arg	Thr	Thr	Val	Ser	Ala	Gln		
				195				200						205			
tct	cgc	ttc	ctc	agt	acc	tat	gat	gga	gca	gag	acg	ctc	tgc	ctg	gag	672	
Ser	Arg	Phe	Leu	Ser	Thr	Tyr	Asp	Gly	Ala	Glu	Thr	Leu	Cys	Leu	Glu		
				210			215							220			
gac	ata	tac	aca	gag	aat	gtc	ctg	gag	gtc	tgg	gca	gat	gtg	ggc	atg	720	
Asp	Ile	Tyr	Thr	Glu	Asn	Val	Leu	Glu	Val	Trp	Ala	Asp	Val	Gly	Met		
225					230					235					240		
gct	gga	ccc	ccg	cag	aag	agc	cca	gcc	acc	ctg	ggc	ctg	gag	gag	ctc	768	
Ala	Gly	Pro	Pro	Gln	Lys	Ser	Pro	Ala	Thr	Leu	Gly	Leu	Glu	Glu	Leu		
				245				250						255			
ttc	agc	acc	cct	ggc	cac	ctc	aat	gac	gat	gcg	gac	act	gtg	ctg	gtg	816	
Phe	Ser	Thr	Pro	Gly	His	Leu	Asn	Asp	Asp	Ala	Asp	Thr	Val	Leu	Val		

260	265	270	
gtg ggt gag gcg ggc agt ggc aag agc acg ctc ctg cag cgg ctg cac			864
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His			
275	280	285	
ttg ctg tgg gct gca ggg caa gac ttc cag gaa ttt ctc ttt gtc ttc			912
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe			
290	295	300	
cca ttc agc tgc cgg cag ctg cag tgc atg gcc aaa cca ctc tct gtg			960
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val			
305	310	315	320
cgg act cta ctc ttt gag cac tgc tgt tgg cct gat gtt ggt caa gaa			1008
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu			
325	330	335	
gac atc ttc cag tta ctc ctt gac cac cct gac cgt gtc ctg tta acc			1056
Asp Ile Phe Gln Leu Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr			
340	345	350	
ttt gat ggc ttt gac gag ttc aag ttc agg ttc acg gat cgt gaa cgc			1104
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg			
355	360	365	
cac tgc tcc ccg acc gac ccc acc tct gtc cag acc ctg ctc ttc aac			1152
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn			
370	375	380	
ctt ctg cag ggc aac ctg ctg aag aat gcc cgc aag gtg gtg acc agc			1200
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser			
385	390	395	400
cgt ccg gcc gct gtg tcg gcg ttc ctc agg aag tac atc cgc acc gag			1248
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu			
405	410	415	
ttc aac ctc aag ggc ttc tct gaa cag ggc atc gag ctg tac ctg agg			1296
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg			
420	425	430	
aag cgc cat cat gag ccc ggg gtg gcg gac cgc ctc atc cgc ctg ctc			1344
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu			
435	440	445	
caa gag acc tca gcc ctg cac ggt ttg tgc cac ctg cct gtc ttc tca			1392
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser			
450	455	460	
tgg atg gtg tcc aaa tgc cac cag gaa ctg ttg ctg cag gag ggg ggg			1440
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Leu Gln Glu Gly Gly			
465	470	475	480

tcc cca aag acc act aca gat atg tac ctg ctg att ctg cag cat ttt 1488  
Ser Pro Lys Thr Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe  
485 490 495

ctg ctg cat gcc acc ccc cca gac tca gct tcc caa ggt ctg gga ccc 1536  
Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro  
500 505 510

agt ctt ctt cgg ggc cgc ctc ccc acc ctc ctg cac ctg ggc aga ctg 1584  
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu  
515 520 525

gct ctg tgg ggc ctg ggc atg tgc tgc tac gtg ttc tca gcc cag cag 1632  
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln  
530 535 540

ctc cag gca gca cag gtc agc cct gat gac att tct ctt ggc ttc ctg 1680  
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu  
545 550 555 560

gtgctgcca aaggtgtcgt gccagggagt acggcgcccc tggaattcct tcacatcact 1740  
ttccagtgtc tctttgccgc gttctacctg gcactcagt ctgatgtgcc accagctttg 1800  
ctcagacacc tcttcaattg tggcaggcca ggcaactcac caatggccag gctcctgccc 1860  
acgatgtgca tccaggcctc ggagggaaag gacagcagcg tggcagcttt gctgcagaag 1920  
gccgagccgc acaaccttca gatcacagca gccttcctgg cagggctgtt gtcccgggag 1980  
cactggggcc tgctggctga gtgccagaca tctgagaagg ccctgctccg gcgccaggcc 2040  
tgtgcccgtc ggtgtctggc ccgcagcctc cgcaagcact tccactccat cccgccagct 2100  
gcaccgggtg aggccaagag cgtgcatgcc atgcccgggt tcatctggct catccggagc 2160  
ctgtacgaga tgcaggagga gcggctggct cggaaggctg cacgtggcct gaatgttggg 2220  
cacctcaagt tgacattttg cagtgtgggc cccactgagt gtgctgccct ggcctttgtg 2280  
ctgcagcacc tccggcggcc cgtggccctg cagctggact acaactctgt gggtgacatt 2340  
ggcgtggagc agctgctgcc ttgccttggg gtctgcaagg ctctgtattt gcgcgataac 2400  
aatatctcag accgaggcat ctgcaagctc attgaatgtg ctcttactg cgagcaattg 2460  
cagaagttag cgctggggaa taactacatc actgccgcgg gagcccaagt gctggccgag 2520  
gggctccgag gcaacacctc cttgcagttc ctgggattct ggggcaacag agtgggtgac 2580  
gagggggccc aggccctggc tgaagccttg ggtgatcacc agagcttgag gtggctcagc 2640  
ctggtgggga acaacatttg cagtgtgggt gcccaagcct tggcactgat gctggcaaag 2700  
aacgtcatgc tagaagaact ctgcctggag gagaaccatc tccaggatga aggtgtatgt 2760  
tctctcgcag aaggactgaa gaaaaattca agtttgaaaa tctgaacat aaaaattcat 2820  
gcttcgggat tcaacaaact cttggaaagc attttctgca tctcctggg tgtggaagca 2880  
tttttctcgc agaaagttgt caagattctt gaagaaatgg tagtcagttg gctagaggct 2940  
aggttggtcca ataactgcat cacctaccta ggggcagaag ccctcctgca ggcccttgaa 3000  
aggaatgaca ccatcctgga agtctggtaa 3030

<210> 83

<211> 560

<212> PRT

<213> Homo sapien

<400> 83

Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu  
1 5 10 15

Val	Glu	Leu	Leu	Val	Ser	Gly	Ser	Leu	Glu	Gly	Phe	Glu	Ser	Val	Leu
		20						25					30		
Asp	Trp	Leu	Leu	Ser	Trp	Glu	Val	Leu	Ser	Trp	Glu	Asp	Tyr	Glu	Gly
		35					40					45			
Phe	His	Leu	Leu	Gly	Gln	Pro	Leu	Ser	His	Leu	Ala	Arg	Arg	Leu	Leu
		50				55					60				
Asp	Thr	Val	Trp	Asn	Lys	Gly	Thr	Trp	Ala	Cys	Gln	Lys	Leu	Ile	Ala
65					70					75				80	
Ala	Ala	Gln	Glu	Ala	Gln	Ala	Asp	Ser	Gln	Ser	Pro	Lys	Leu	His	Gly
				85					90					95	
Cys	Trp	Asp	Pro	His	Ser	Leu	His	Pro	Ala	Arg	Asp	Leu	Gln	Ser	His
			100					105					110		
Arg	Pro	Ala	Ile	Val	Arg	Arg	Leu	His	Ser	His	Val	Glu	Asn	Met	Leu
		115					120					125			
Asp	Leu	Ala	Trp	Glu	Arg	Gly	Phe	Val	Ser	Gln	Tyr	Glu	Cys	Asp	Glu
		130				135					140				
Ile	Arg	Leu	Pro	Ile	Phe	Thr	Pro	Ser	Gln	Arg	Ala	Arg	Arg	Leu	Leu
145					150					155				160	
Asp	Leu	Ala	Thr	Val	Lys	Ala	Asn	Gly	Leu	Ala	Ala	Phe	Leu	Leu	Gln
				165					170					175	
His	Val	Gln	Glu	Leu	Pro	Val	Pro	Leu	Ala	Leu	Pro	Leu	Glu	Ala	Ala
			180					185					190		
Thr	Cys	Lys	Lys	Tyr	Met	Ala	Lys	Leu	Arg	Thr	Thr	Val	Ser	Ala	Gln
		195					200					205			
Ser	Arg	Phe	Leu	Ser	Thr	Tyr	Asp	Gly	Ala	Glu	Thr	Leu	Cys	Leu	Glu
		210				215					220				
Asp	Ile	Tyr	Thr	Glu	Asn	Val	Leu	Glu	Val	Trp	Ala	Asp	Val	Gly	Met
225					230					235				240	
Ala	Gly	Pro	Pro	Gln	Lys	Ser	Pro	Ala	Thr	Leu	Gly	Leu	Glu	Glu	Leu
				245					250					255	
Phe	Ser	Thr	Pro	Gly	His	Leu	Asn	Asp	Asp	Ala	Asp	Thr	Val	Leu	Val
			260					265					270		
Val	Gly	Glu	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Gln	Arg	Leu	His
		275					280					285			
Leu	Leu	Trp	Ala	Ala	Gly	Gln	Asp	Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe
		290				295				300					
Pro	Phe	Ser	Cys	Arg	Gln	Leu	Gln	Cys	Met	Ala	Lys	Pro	Leu	Ser	Val
305					310					315				320	
Arg	Thr	Leu	Leu	Phe	Glu	His	Cys	Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu
				325					330					335	
Asp	Ile	Phe	Gln	Leu	Leu	Leu	Asp	His	Pro	Asp	Arg	Val	Leu	Leu	Thr
			340					345					350		
Phe	Asp	Gly	Phe	Asp	Glu	Phe	Lys	Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg
		355					360					365			
His	Cys	Ser	Pro	Thr	Asp	Pro	Thr	Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn
			370			375					380				
Leu	Leu	Gln	Gly	Asn	Leu	Leu	Lys	Asn	Ala	Arg	Lys	Val	Val	Thr	Ser
385					390					395				400	
Arg	Pro	Ala	Ala	Val	Ser	Ala	Phe	Leu	Arg	Lys	Tyr	Ile	Arg	Thr	Glu
				405					410					415	
Phe	Asn	Leu	Lys	Gly	Phe	Ser	Glu	Gln	Gly	Ile	Glu	Leu	Tyr	Leu	Arg
			420					425					430		
Lys	Arg	His	His	Glu	Pro	Gly	Val	Ala	Asp	Arg	Leu	Ile	Arg	Leu	Leu



435	440	445
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser		
450	455	460
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Leu Gln Glu Gly Gly		
465	470	475
Ser Pro Lys Thr Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe		
	485	490
Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro		
	500	505
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu		
	515	520
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln		
	530	535
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu		
545	550	555
		560

<210> 84  
 <211> 1107  
 <212> DNA  
 <213> Homo sapien

<400> 84  
 attctttttt taacttttac ttattcatta ggatgatttc ataatatatt tcctgggttta 60  
 gaggaacag gaacaatggc taccgagagt actccctcag agatcataga aagagaaaga 120  
 aaaaagttgc ttgaaatcct tcaacatgat cctgattcta tcttagacac gttaacttct 180  
 cggaggctga tttctgagga agagtatgag actctggaga atgttacaga tctcctgaag 240  
 aaaagtcgga agctgttaat tttggtacag aaaaaggagaggcgcactg tcagcatttt 300  
 ctcaagtgtt tatttagtac ttttccacag tcagctgcca tttgcggctt aaggcatgaa 360  
 gttttaaaac atgagaatac agtacctcct caatctatgg gggcaagcag taattcagaa 420  
 gatgcttttt ctcttggaat aaaacagcct gaagcccctg agatcacagt gttcttcagt 480  
 gagaaggaac acttggtatt ggaaacctct gagtttttca gggacaagaa aactagttat 540  
 agggaaacag ctttgtctgc caggaagaat gagaaggaat atgacacacc agaagtcaca 600  
 ttatcatatt cagttgagaa agttggatgt gaagttccag caactattac atatataaaa 660  
 gatggacaga gatatgagga gctagatgat tctttatact taggaaaaga ggaatatcta 720  
 ggatctgttg acaccctga agatgcagaa gccactgtgg aagaggaggt ttatgatgac 780  
 ccagagcacg ttggatatga tggatgaagag gacttcgaga attcagaaac cacagagttc 840  
 tctggtgaag aaccaagtta tgagggatca gaaaccagcc tttcattgga ggaggaacag 900  
 gagaaaagta tagaaggctg gtctcgaact catgggctta agcgatcctc ccacgttggc 960  
 ctcccaaagt gctgggatta caggcgtgag ccaccctgcc tggcctgaaa attctgcctc 1020  
 aaacatctca aacatccatt tatattttgt acaagaaagt aaataaaaatt tttcttttta 1080  
 acattaaaaa aaaaaaaaaa aaaaaaa 1107

<210> 85  
 <211> 510  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> CDS  
 <222> (15)...(305)

<400> 85

```

aggagagaaaa agcc atg gcc gac aag gtc ctg aag gag aag aga aag ctg 50
                Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu
                  1             5             10

ttt atc cat tcc atg ggt gaa ggt aca ata aat ggc tta ctg gat gaa 98
Phe Ile His Ser Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu
      15             20             25

tta tta cag aca agg gtg ctg aac cag gaa gag atg gag aaa gta aaa 146
Leu Leu Gln Thr Arg Val Leu Asn Gln Glu Glu Met Glu Lys Val Lys
      30             35             40

cgt gaa aat gct aca gtt atg gat aag acc cga gct ttg att gac tcc 194
Arg Glu Asn Ala Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser
      45             50             55             60

gtt att ccg aaa ggg gca cag gca tgc caa att tgc atc aca tac att 242
Val Ile Pro Lys Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile
      65             70             75

tgt gaa gaa gac agt tac ctg gca gag acg ctg gga ctc tca gca ggt 290
Cys Glu Glu Asp Ser Tyr Leu Ala Glu Thr Leu Gly Leu Ser Ala Gly
      80             85             90

ccg ata cct gga aat tagcttagct tagtacacaa gactcccaat tactatttttc 345
Pro Ile Pro Gly Asn
      95

ttccttccca gctcttcagg cagtgcagga caaccagct atgccacat gctcaagccc 405
agaaggcaga atcaagcttt gctttctaga agacgctcaa aggatatgga aacaaaagtt 465
gcagaggtgc catgttcaga atacaataat aaagtggagt aaaga 510

<210> 86
<211> 97
<212> PRT
<213> Homo sapien

<400> 86
Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile His Ser
 1             5             10             15
Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr
      20             25             30
Arg Val Leu Asn Gln Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala
      35             40             45
Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys
      50             55             60
Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp
      65             70             75             80
Ser Tyr Leu Ala Glu Thr Leu Gly Leu Ser Ala Gly Pro Ile Pro Gly
      85             90             95
Asn

```

<210> 87  
 <211> 97  
 <212> PRT  
 <213> Homo sapien

<400> 87  
 Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile Arg Ser  
 1 5 10 15  
 Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr  
 20 25 30  
 Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala  
 35 40 45  
 Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys  
 50 55 60  
 Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp  
 65 70 75 80  
 Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Asp Gln Thr Ser Gly  
 85 90 95  
 Asn

<210> 88

<400> 88  
 000

<210> 89  
 <211> 321  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> CDS  
 <222> (1)...(318)

<400> 89  
 atg atc ctc ctg aag aag aga cgg ctg ctt atc aat tca ttg ggt gaa 48  
 Met Ile Leu Leu Lys Lys Arg Arg Leu Leu Ile Asn Ser Leu Gly Glu  
 1 5 10 15  
 ggt aca ata aat ggc tta ctg gat gaa tta ttg gag aca aat gtg ctg 96  
 Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Glu Thr Asn Val Leu  
 20 25 30  
 agc cag gaa gac aca gag ata gta aaa tgt gaa aat gtt aca gtt atc 144  
 Ser Gln Glu Asp Thr Glu Ile Val Lys Cys Glu Asn Val Thr Val Ile  
 35 40 45  
 gat aag gcc cga gat ttg ctt gac tct gtt att cgg aaa ggg gca ggg 192  
 Asp Lys Ala Arg Asp Leu Leu Asp Ser Val Ile Arg Lys Gly Ala Gly  
 50 55 60

gca tgt gaa att tgc atc aca tac att tgt gaa gaa gac agg tac ctg 240  
Ala Cys Glu Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp Arg Tyr Leu  
65 70 75 80

gca ggg acg ctg gga ctc tca gca gga aat gac tac aga gct gga ggc 288  
Ala Gly Thr Leu Gly Leu Ser Ala Gly Asn Asp Tyr Arg Ala Gly Gly  
85 90 95

att tgc tca ccg ccc aga gca caa gac ctc tga 321  
Ile Cys Ser Pro Pro Arg Ala Gln Asp Leu  
100 105

<210> 90  
<211> 106  
<212> PRT  
<213> Homo sapien

<400> 90  
Met Ile Leu Leu Lys Lys Arg Arg Leu Leu Ile Asn Ser Leu Gly Glu  
1 5 10 15  
Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Glu Thr Asn Val Leu  
20 25 30  
Ser Gln Glu Asp Thr Glu Ile Val Lys Cys Glu Asn Val Thr Val Ile  
35 40 45  
Asp Lys Ala Arg Asp Leu Leu Asp Ser Val Ile Arg Lys Gly Ala Gly  
50 55 60  
Ala Cys Glu Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp Arg Tyr Leu  
65 70 75 80  
Ala Gly Thr Leu Gly Leu Ser Ala Gly Asn Asp Tyr Arg Ala Gly Gly  
85 90 95  
Ile Cys Ser Pro Pro Arg Ala Gln Asp Leu  
100 105

<210> 91  
<211> 108  
<212> PRT  
<213> Homo sapien

<400> 91  
Met Ala Asp Lys Val Leu Leu Glu Lys Arg Lys Leu Leu Ile Asn Ser  
1 5 10 15  
Leu Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Glu Thr  
20 25 30  
Asn Val Leu Ser Gln Glu Asp Glu Ile Val Lys Arg Glu Asn Ala Thr  
35 40 45  
Val Ile Asp Lys Ala Arg Ala Leu Leu Asp Ser Val Ile Arg Lys Gly  
50 55 60  
Ala Gly Ala Cys Glu Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp Ser  
65 70 75 80  
Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Gly Asn Ala Val Gln Ala

				85					90			95
Gly	Gly	Ala	Cys	Ser	Thr	Ser	Ser	Gly	Gln	Asp	Leu	
			100					105				

<210> 92

<400> 92  
000

<210> 93

<400> 93  
000

<210> 94

<400> 94  
000

<210> 95

<400> 95  
000

<210> 96

<211> 3396

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (277)...(3348)

<400> 96

cgccccgggca ggtgtttata ctccggaggg tgtccccgtg cgtcatcggt ggagtggacc	60
aaaactggtg atctgtttgc cctgtgtgac cttgcccaga accctgctga ctgagagaac	120
acatctgctg gaagtcctct gggattcaag gtacagggaa tgaagagtag ttttacagaa	180
aaaagaggac aatattggga tcacctttga cttttccatt tggaaataat attttctatt	240
gtgttataga aaggtgggaa gctttcatcc agaaca atg aat ttc ata aag gac	294
Met Asn Phe Ile Lys Asp	
1 5	

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa	342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln	
10 15 20	

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta	390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val	
25 30 35	

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc	438
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile	

40	45	50	
att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt			486
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu			
55	60	65	70
aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga			534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly			
75	80		85
caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct			582
Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala			
90	95		100
cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat			630
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr			
105	110		115
ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc			678
Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys Ser Thr Phe			
120	125		130
aca gaa cct atc ctg tgg agg aag gac caa cac cat cac cgc gtg gag			726
Thr Glu Pro Ile Leu Trp Arg Lys Asp Gln His His His Arg Val Glu			
135	140	145	150
cag ctg acc ctg aat ggc ctc ctg cag gct ctt cag agc ccc tgc atc			774
Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser Pro Cys Ile			
155	160		165
att gaa ggg gaa tct ggc aaa ggc aag tcc act ctg ctg cag cgc att			822
Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser Thr Leu Leu Gln Arg Ile			
170	175		180
gcc atg ctc tgg ggc tcc gga aag tgc aag gct ctg acc aag ttc aaa			870
Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr Lys Phe Lys			
185	190		195
ttc gtc ttc ttc ctc cgt ctc agc agg gcc cag ggt gga ctt ttt gaa			918
Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Gly Leu Phe Glu			
200	205		210
acc ctc tgt gat caa ctc ctg gat ata cct ggc aca atc agg aag cag			966
Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro Gly Thr Ile Arg Lys Gln			
215	220	225	230
aca ttc atg gcc atg ctg ctg aag ctg cgg cag agg gtt ctt ttc ctt			1014
Thr Phe Met Ala Met Leu Leu Lys Leu Arg Gln Arg Val Leu Phe Leu			
235	240		245
ctt gat ggc tac aat gaa ttc aag ccc cag aac tgc cca gaa atc gaa			1062
Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln Asn Cys Pro Glu Ile Glu			
250	255		260

gcc ctg ata aag gaa aac cac cgc ttc aag aac atg gtc atc gtc acc	1110
Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val Ile Val Thr	
265 270 275	
act acc act gag tgc ctg agg cac ata cgg cag ttt ggt gcc ctg act	1158
Thr Thr Thr Glu Cys Leu Arg His Ile Arg Gln Phe Gly Ala Leu Thr	
280 285 290	
gct gag gtg ggg gat atg aca gaa gac agc gcc cag gct ctc atc cga	1206
Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala Leu Ile Arg	
295 300 305 310	
gaa gtg ctg atc aag gag ctt gct gaa ggc ttg ttg ctc caa att cag	1254
Glu Val Leu Ile Lys Glu Leu Ala Glu Gly Leu Leu Leu Gln Ile Gln	
315 320 325	
aaa tcc agg tgc ttg agg aat ctc atg aag acc cct ctc ttt gtg gtc	1302
Lys Ser Arg Cys Leu Arg Asn Leu Met Lys Thr Pro Leu Phe Val Val	
330 335 340	
atc act tgt gca atc cag atg ggt gaa agt gag ttc cac tct cac aca	1350
Ile Thr Cys Ala Ile Gln Met Gly Glu Ser Glu Phe His Ser His Thr	
345 350 355	
caa aca acg ctg ttc cat acc ttc tat gat ctg ttg ata cag aaa aac	1398
Gln Thr Thr Leu Phe His Thr Phe Tyr Asp Leu Leu Ile Gln Lys Asn	
360 365 370	
aaa cac aaa cat aaa ggt gtg gct gca agt gac ttc att cgg agc ctg	1446
Lys His Lys His Lys Gly Val Ala Ala Ser Asp Phe Ile Arg Ser Leu	
375 380 385 390	
gac cac cgt gga gac cta gct ctg gag ggt gtg ttc tcc cac aag ttt	1494
Asp His Arg Gly Asp Leu Ala Leu Glu Gly Val Phe Ser His Lys Phe	
395 400 405	
gat ttc gaa ctg cag gat gtg tcc agc gtg aat gag gat gtc ctg ctg	1542
Asp Phe Glu Leu Gln Asp Val Ser Ser Val Asn Glu Asp Val Leu Leu	
410 415 420	
aca act ggg ctc ctc tgt aaa tat aca gct caa agg ttc aag cca aag	1590
Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala Gln Arg Phe Lys Pro Lys	
425 430 435	
tat aaa ttc ttt cac aag tca ttc cag gag tac aca gca gga cga aga	1638
Tyr Lys Phe Phe His Lys Ser Phe Gln Glu Tyr Thr Ala Gly Arg Arg	
440 445 450	
ctc agc agt tta ttg acg tct cat gag cca gag gag gtg acc aag ggg	1686
Leu Ser Ser Leu Leu Thr Ser His Glu Pro Glu Glu Val Thr Lys Gly	
455 460 465 470	

aat ggt tac ttg cag aaa atg gtt tcc att tcg gac att aca tcc act	1734
Asn Gly Tyr Leu Gln Lys Met Val Ser Ile Ser Asp Ile Thr Ser Thr	
475 480 485	
tat agc agc ctg ctc cgg tac acc tgt ggg tca tct gtg gaa gcc acc	1782
Tyr Ser Ser Leu Leu Arg Tyr Thr Cys Gly Ser Ser Val Glu Ala Thr	
490 495 500	
agg gct gtt atg aag cac ctc gca gca gtg tat caa cac ggc tgc ctt	1830
Arg Ala Val Met Lys His Leu Ala Ala Val Tyr Gln His Gly Cys Leu	
505 510 515	
ctc gga ctt tcc atc gcc aag agg cct ctc tgg aga cag gaa tct ttg	1878
Leu Gly Leu Ser Ile Ala Lys Arg Pro Leu Trp Arg Gln Glu Ser Leu	
520 525 530	
caa agt gtg aaa aac acc act gag caa gaa att ctg aaa gcc ata aac	1926
Gln Ser Val Lys Asn Thr Thr Glu Gln Glu Ile Leu Lys Ala Ile Asn	
535 540 545 550	
atc aat tcc ttt gta gag tgt ggc atc cat tta tat caa gag agt aca	1974
Ile Asn Ser Phe Val Glu Cys Gly Ile His Leu Tyr Gln Glu Ser Thr	
555 560 565	
tcc aaa tca gcc ctg agc caa gaa ttt gaa gct ttc ttt caa ggt aaa	2022
Ser Lys Ser Ala Leu Ser Gln Glu Phe Glu Ala Phe Phe Gln Gly Lys	
570 575 580	
agc tta tat atc aac tca ggg aac atc ccc gat tac tta ttt gac ttc	2070
Ser Leu Tyr Ile Asn Ser Gly Asn Ile Pro Asp Tyr Leu Phe Asp Phe	
585 590 595	
ttt gaa cat ttg ccc aat tgt gca agt gcc ctg gac ttc att aaa ctg	2118
Phe Glu His Leu Pro Asn Cys Ala Ser Ala Leu Asp Phe Ile Lys Leu	
600 605 610	
gac ttt tat ggg gga gct atg gct tca tgg gaa aag gct gca gaa gac	2166
Asp Phe Tyr Gly Gly Ala Met Ala Ser Trp Glu Lys Ala Ala Glu Asp	
615 620 625 630	
aca ggt gga atc cac atg gaa gag gcc cca gaa acc tac att ccc agc	2214
Thr Gly Gly Ile His Met Glu Glu Ala Pro Glu Thr Tyr Ile Pro Ser	
635 640 645	
agg gct gta tct ttg ttc ttc aac tgg aag cag gaa ttc agg act ctg	2262
Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln Glu Phe Arg Thr Leu	
650 655 660	
gag gtc aca ctc cgg gat ttc agc aag ttg aat aag caa gat atc aga	2310
Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn Lys Gln Asp Ile Arg	
665 670 675	
tat ctg ggg aaa ata ttc agc tct gcc aca agc ctc agg ctg caa ata	2358



Tyr	Leu	Gly	Lys	Ile	Phe	Ser	Ser	Ala	Thr	Ser	Leu	Arg	Leu	Gln	Ile		
680						685					690						
aag	aga	tgt	gct	ggg	gtg	gct	gga	agc	ctc	agt	ttg	gtc	ctc	agc	acc	2406	
Lys	Arg	Cys	Ala	Gly	Val	Ala	Gly	Ser	Leu	Ser	Leu	Val	Leu	Ser	Thr		
695					700					705					710		
tgt	aag	aac	att	tat	tct	ctc	atg	gtg	gaa	gcc	agt	ccc	ctc	acc	ata	2454	
Cys	Lys	Asn	Ile	Tyr	Ser	Leu	Met	Val	Glu	Ala	Ser	Pro	Leu	Thr	Ile		
			715						720					725			
gaa	gat	gag	agg	cac	atc	aca	tct	gta	aca	aac	ctg	aaa	acc	ttg	agt	2502	
Glu	Asp	Glu	Arg	His	Ile	Thr	Ser	Val	Thr	Asn	Leu	Lys	Thr	Leu	Ser		
			730					735					740				
att	cat	gac	cta	cag	aat	caa	cgg	ctg	ccg	ggg	ggg	ctg	act	gac	agc	2550	
Ile	His	Asp	Leu	Gln	Asn	Gln	Arg	Leu	Pro	Gly	Gly	Leu	Thr	Asp	Ser		
		745					750						755				
ttg	ggg	aac	ttg	aag	aac	ctt	aca	aag	ctc	ata	atg	gat	aac	ata	aag	2598	
Leu	Gly	Asn	Leu	Lys	Asn	Leu	Thr	Lys	Leu	Ile	Met	Asp	Asn	Ile	Lys		
	760					765					770						
atg	aat	gaa	gaa	gat	gct	ata	aaa	cta	gct	gaa	ggc	ctg	aaa	aac	ctg	2646	
Met	Asn	Glu	Glu	Asp	Ala	Ile	Lys	Leu	Ala	Glu	Gly	Leu	Lys	Asn	Leu		
	775				780					785					790		
aag	aag	atg	tgt	tta	ttt	cat	ttg	acc	cac	ttg	tct	gac	att	gga	gag	2694	
Lys	Lys	Met	Cys	Leu	Phe	His	Leu	Thr	His	Leu	Ser	Asp	Ile	Gly	Glu		
			795						800					805			
gga	atg	gat	tac	ata	gtc	aag	tct	ctg	tca	agt	gaa	ccc	tgt	gac	ctt	2742	
Gly	Met	Asp	Tyr	Ile	Val	Lys	Ser	Leu	Ser	Ser	Glu	Pro	Cys	Asp	Leu		
			810					815					820				
gaa	gaa	att	caa	tta	gtc	tcc	tgc	tgc	ttg	tct	gca	aat	gca	gtg	aaa	2790	
Glu	Glu	Ile	Gln	Leu	Val	Ser	Cys	Cys	Leu	Ser	Ala	Asn	Ala	Val	Lys		
		825					830					835					
atc	cta	gct	cag	aat	ctt	cac	aat	ttg	gtc	aaa	ctg	agc	att	ctt	gat	2838	
Ile	Leu	Ala	Gln	Asn	Leu	His	Asn	Leu	Val	Lys	Leu	Ser	Ile	Leu	Asp		
	840					845					850						
tta	tca	gaa	aat	tac	ctg	gaa	aaa	gat	gga	aat	gaa	gct	ctt	cat	gaa	2886	
Leu	Ser	Glu	Asn	Tyr	Leu	Glu	Lys	Asp	Gly	Asn	Glu	Ala	Leu	His	Glu		
	855				860					865					870		
ctg	atc	gac	agg	atg	aac	gtg	cta	gaa	cag	ctc	acc	gca	ctg	atg	ctg	2934	
Leu	Ile	Asp	Arg	Met	Asn	Val	Leu	Glu	Gln	Leu	Thr	Ala	Leu	Met	Leu		
			875					880					885				
ccc	tgg	ggc	tgt	gac	gtg	caa	ggc	agc	ctg	agc	agc	ctg	ttg	aaa	cat	2982	
Pro	Trp	Gly	Cys	Asp	Val	Gln	Gly	Ser	Leu	Ser	Ser	Leu	Leu	Lys	His		

890	895	900	
ttg gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga			3030
Leu Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg			
905	910	915	
ctc aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac			3078
Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn			
920	925	930	
cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc			3126
Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser			
935	940	945	950
agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag caa			3174
Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln			
955	960	965	
tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct gat cca gca			3222
Leu Val Phe Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala			
970	975	980	
tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act ttt ctg caa			3270
Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln			
985	990	995	
gaa gct agg ctt gtt ggg tgg caa ttt gat gat gat gat ctc agt gtt			3318
Glu Ala Arg Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val			
1000	1005	1010	
att aca ggt gct ttt aaa cta gta act gct taaataaagt gtactcgaag			3368
Ile Thr Gly Ala Phe Lys Leu Val Thr Ala			
1015	1020		
ccaaaaaaaa aaaaaaaaaa aaaaaaaaa			3396
<210> 97			
<211> 1024			
<212> PRT			
<213> Homo sapien			
<400> 97			
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly			
1 5 10 15			
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val			
20 25 30			
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln			
35 40 45			
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu			
50 55 60			
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu			
65 70 75 80			
Phe Gln Asp Leu Asn Gly Gln Ser Leu Phe His Gln Thr Ser Glu Gly			

85																90																95															
Asp	Leu	Asp	Asp	Leu	Ala	Gln	Asp	Leu	Lys	Asp	Leu	Tyr	His	Thr	Pro																																
100								105								110																															
Ser	Phe	Leu	Asn	Phe	Tyr	Pro	Leu	Gly	Glu	Asp	Ile	Asp	Ile	Ile	Phe																																
115								120								125																															
Asn	Leu	Lys	Ser	Thr	Phe	Thr	Glu	Pro	Ile	Leu	Trp	Arg	Lys	Asp	Gln																																
130								135								140																															
His	His	His	Arg	Val	Glu	Gln	Leu	Thr	Leu	Asn	Gly	Leu	Leu	Gln	Ala																																
145	150								155								160																														
Leu	Gln	Ser	Pro	Cys	Ile	Ile	Glu	Gly	Glu	Ser	Gly	Lys	Gly	Lys	Ser																																
165								170								175																															
Thr	Leu	Leu	Gln	Arg	Ile	Ala	Met	Leu	Trp	Gly	Ser	Gly	Lys	Cys	Lys																																
180								185								190																															
Ala	Leu	Thr	Lys	Phe	Lys	Phe	Val	Phe	Phe	Leu	Arg	Leu	Ser	Arg	Ala																																
195								200								205																															
Gln	Gly	Gly	Leu	Phe	Glu	Thr	Leu	Cys	Asp	Gln	Leu	Leu	Asp	Ile	Pro																																
210								215								220																															
Gly	Thr	Ile	Arg	Lys	Gln	Thr	Phe	Met	Ala	Met	Leu	Leu	Lys	Leu	Arg																																
225	230								235								240																														
Gln	Arg	Val	Leu	Phe	Leu	Leu	Asp	Gly	Tyr	Asn	Glu	Phe	Lys	Pro	Gln																																
245								250								255																															
Asn	Cys	Pro	Glu	Ile	Glu	Ala	Leu	Ile	Lys	Glu	Asn	His	Arg	Phe	Lys																																
260								265								270																															
Asn	Met	Val	Ile	Val	Thr	Thr	Thr	Thr	Glu	Cys	Leu	Arg	His	Ile	Arg																																
275								280								285																															
Gln	Phe	Gly	Ala	Leu	Thr	Ala	Glu	Val	Gly	Asp	Met	Thr	Glu	Asp	Ser																																
290								295								300																															
Ala	Gln	Ala	Leu	Ile	Arg	Glu	Val	Leu	Ile	Lys	Glu	Leu	Ala	Glu	Gly																																
305	310								315								320																														
Leu	Leu	Leu	Gln	Ile	Gln	Lys	Ser	Arg	Cys	Leu	Arg	Asn	Leu	Met	Lys																																
325								330								335																															
Thr	Pro	Leu	Phe	Val	Val	Ile	Thr	Cys	Ala	Ile	Gln	Met	Gly	Glu	Ser																																
340								345								350																															
Glu	Phe	His	Ser	His	Thr	Gln	Thr	Thr	Leu	Phe	His	Thr	Phe	Tyr	Asp																																
355								360								365																															
Leu	Leu	Ile	Gln	Lys	Asn	Lys	His	Lys	His	Lys	Gly	Val	Ala	Ala	Ser																																
370								375								380																															
Asp	Phe	Ile	Arg	Ser	Leu	Asp	His	Arg	Gly	Asp	Leu	Ala	Leu	Glu	Gly																																
385	390								395								400																														
Val	Phe	Ser	His	Lys	Phe	Asp	Phe	Glu	Leu	Gln	Asp	Val	Ser	Ser	Val																																
405								410								415																															
Asn	Glu	Asp	Val	Leu	Leu	Thr	Thr	Gly	Leu	Leu	Cys	Lys	Tyr	Thr	Ala																																
420								425								430																															
Gln	Arg	Phe	Lys	Pro	Lys	Tyr	Lys	Phe	His	Lys	Ser	Phe	Gln	Glu																																	
435								440								445																															
Tyr	Thr	Ala	Gly	Arg	Arg	Leu	Ser	Ser	Leu	Leu	Thr	Ser	His	Glu	Pro																																
450								455								460																															
Glu	Glu	Val	Thr	Lys	Gly	Asn	Gly	Tyr	Leu	Gln	Lys	Met	Val	Ser	Ile																																
465	470								475								480																														
Ser	Asp	Ile	Thr	Ser	Thr	Tyr	Ser	Ser	Leu	Leu	Arg	Tyr	Thr	Cys	Gly																																
485								490								495																															
Ser	Ser	Val	Glu	Ala	Thr	Arg	Ala	Val	Met	Lys	His	Leu	Ala	Ala	Val																																
500								505								510																															

Tyr	Gln	His	Gly	Cys	Leu	Leu	Gly	Leu	Ser	Ile	Ala	Lys	Arg	Pro	Leu	515	520	525
Trp	Arg	Gln	Glu	Ser	Leu	Gln	Ser	Val	Lys	Asn	Thr	Thr	Glu	Gln	Glu	530	535	540
Ile	Leu	Lys	Ala	Ile	Asn	Ile	Asn	Ser	Phe	Val	Glu	Cys	Gly	Ile	His	545	550	555
Leu	Tyr	Gln	Glu	Ser	Thr	Ser	Lys	Ser	Ala	Leu	Ser	Gln	Glu	Phe	Glu	565	570	575
Ala	Phe	Phe	Gln	Gly	Lys	Ser	Leu	Tyr	Ile	Asn	Ser	Gly	Asn	Ile	Pro	580	585	590
Asp	Tyr	Leu	Phe	Asp	Phe	Phe	Glu	His	Leu	Pro	Asn	Cys	Ala	Ser	Ala	595	600	605
Leu	Asp	Phe	Ile	Lys	Leu	Asp	Phe	Tyr	Gly	Gly	Ala	Met	Ala	Ser	Trp	610	615	620
Glu	Lys	Ala	Ala	Glu	Asp	Thr	Gly	Gly	Ile	His	Met	Glu	Glu	Ala	Pro	625	630	635
Glu	Thr	Tyr	Ile	Pro	Ser	Arg	Ala	Val	Ser	Leu	Phe	Phe	Asn	Trp	Lys	645	650	655
Gln	Glu	Phe	Arg	Thr	Leu	Glu	Val	Thr	Leu	Arg	Asp	Phe	Ser	Lys	Leu	660	665	670
Asn	Lys	Gln	Asp	Ile	Arg	Tyr	Leu	Gly	Lys	Ile	Phe	Ser	Ser	Ala	Thr	675	680	685
Ser	Leu	Arg	Leu	Gln	Ile	Lys	Arg	Cys	Ala	Gly	Val	Ala	Gly	Ser	Leu	690	695	700
Ser	Leu	Val	Leu	Ser	Thr	Cys	Lys	Asn	Ile	Tyr	Ser	Leu	Met	Val	Glu	705	710	715
Ala	Ser	Pro	Leu	Thr	Ile	Glu	Asp	Glu	Arg	His	Ile	Thr	Ser	Val	Thr	725	730	735
Asn	Leu	Lys	Thr	Leu	Ser	Ile	His	Asp	Leu	Gln	Asn	Gln	Arg	Leu	Pro	740	745	750
Gly	Gly	Leu	Thr	Asp	Ser	Leu	Gly	Asn	Leu	Lys	Asn	Leu	Thr	Lys	Leu	755	760	765
Ile	Met	Asp	Asn	Ile	Lys	Met	Asn	Glu	Glu	Asp	Ala	Ile	Lys	Leu	Ala	770	775	780
Glu	Gly	Leu	Lys	Asn	Leu	Lys	Lys	Met	Cys	Leu	Phe	His	Leu	Thr	His	785	790	795
Leu	Ser	Asp	Ile	Gly	Glu	Gly	Met	Asp	Tyr	Ile	Val	Lys	Ser	Leu	Ser	805	810	815
Ser	Glu	Pro	Cys	Asp	Leu	Glu	Glu	Ile	Gln	Leu	Val	Ser	Cys	Cys	Leu	820	825	830
Ser	Ala	Asn	Ala	Val	Lys	Ile	Leu	Ala	Gln	Asn	Leu	His	Asn	Leu	Val	835	840	845
Lys	Leu	Ser	Ile	Leu	Asp	Leu	Ser	Glu	Asn	Tyr	Leu	Glu	Lys	Asp	Gly	850	855	860
Asn	Glu	Ala	Leu	His	Glu	Leu	Ile	Asp	Arg	Met	Asn	Val	Leu	Glu	Gln	865	870	875
Leu	Thr	Ala	Leu	Met	Leu	Pro	Trp	Gly	Cys	Asp	Val	Gln	Gly	Ser	Leu	885	890	895
Ser	Ser	Leu	Leu	Lys	His	Leu	Glu	Glu	Val	Pro	Gln	Leu	Val	Lys	Leu	900	905	910
Gly	Leu	Lys	Asn	Trp	Arg	Leu	Thr	Asp	Thr	Glu	Ile	Arg	Ile	Leu	Gly	915	920	925
Ala	Phe	Phe	Gly	Lys	Asn	Pro	Leu	Lys	Asn	Phe	Gln	Gln	Leu	Asn	Leu			

930	935	940
Ala Gly Asn Arg Val Ser Ser Asp Gly Trp Leu	Ala Phe Met Gly Val	
945	950	955
Phe Glu Asn Leu Lys Gln Leu Val Phe Phe Asp Phe Ser Thr Lys Glu		960
	965	970
Phe Leu Pro Asp Pro Ala Leu Val Arg Lys Leu Ser Gln Val Leu Ser		975
	980	985
Lys Leu Thr Phe Leu Gln Glu Ala Arg Leu Val Gly Trp Gln Phe Asp		990
	995	1000
Asp Asp Asp Leu Ser Val Ile Thr Gly Ala Phe Lys Leu Val Thr Ala		1005
1010	1015	1020

<210> 98  
<211> 1395  
<212> DNA  
<213> Homo sapien

<220>  
<221> CDS  
<222> (277) ... (1353)

<400> 98  
cgcccgggca ggtgtttata ctccggaggg tgtccccgtg cgtcatcggt ggagtggacc 60  
aaaactggtg atctgtttgc cctgtgtgac cttgcccgaga accctgctga ctgagagaac 120  
acatctgctg gaagtcctct gggattcaag gtacagggaa tgaagagtag ttttacagaa 180  
aaaagaggac aatattggga tcacctttga cttttccatt tggaaataat attttctatt 240  
gtgttataga aagggtgggaa gctttcatcc agaaca atg aat ttc ata aag gac 294  
Met Asn Phe Ile Lys Asp  
1 5  
  
aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342  
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln  
10 15 20  
  
atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390  
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val  
25 30 35  
  
aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438  
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile  
40 45 50  
  
att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 486  
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu  
55 60 65 70  
  
aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534  
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly  
75 80 85  
  
caa agt ggt ctg act gac agc ttg ggt aac ttg aag aac ctt aca aag 582  
Gln Ser Gly Leu Thr Asp Ser Leu Gly Asn Leu Lys Asn Leu Thr Lys

90	95	100	
ctc ata atg gat aac ata aag atg aat gaa gaa gat gct ata aaa cta			630
Leu Ile Met Asp Asn Ile Lys Met Asn Glu Glu Asp Ala Ile Lys Leu			
105	110	115	
gct gaa ggc ctg aaa aac ctg aag aag atg tgt tta ttt cat ttg acc			678
Ala Glu Gly Leu Lys Asn Leu Lys Lys Met Cys Leu Phe His Leu Thr			
120	125	130	
cac ttg tct gac att gga gag gga atg gat tac ata gtc aag tct ctg			726
His Leu Ser Asp Ile Gly Glu Gly Met Asp Tyr Ile Val Lys Ser Leu			
135	140	145	150
tca agt gaa ccc tgt gac ctt gaa gaa att caa tta gtc tcc tgc tgc			774
Ser Ser Glu Pro Cys Asp Leu Glu Glu Ile Gln Leu Val Ser Cys Cys			
155	160	165	
ttg tct gca aat gca gtg aaa atc cta gct cag aat ctt cac aat ttg			822
Leu Ser Ala Asn Ala Val Lys Ile Leu Ala Gln Asn Leu His Asn Leu			
170	175	180	
gtc aaa ctg agc att ctt gat tta tca gaa aat tac ctg gaa aaa gat			870
Val Lys Leu Ser Ile Leu Asp Leu Ser Glu Asn Tyr Leu Glu Lys Asp			
185	190	195	
gga aat gaa gct ctt cat gaa ctg atc gac agg atg aac gtg cta gaa			918
Gly Asn Glu Ala Leu His Glu Leu Ile Asp Arg Met Asn Val Leu Glu			
200	205	210	
cag ctc acc gca ctg atg ctg ccc tgg ggc tgt gac gtg caa ggc agc			966
Gln Leu Thr Ala Leu Met Leu Pro Trp Gly Cys Asp Val Gln Gly Ser			
215	220	225	230
ctg agc agc ctg ttg aaa cat ttg gag gag gtc cca caa ctc gtc aag			1014
Leu Ser Ser Leu Leu Lys His Leu Glu Glu Val Pro Gln Leu Val Lys			
235	240	245	
ctt ggg ttg aaa aac tgg aga ctc aca gat aca gag att aga att tta			1062
Leu Gly Leu Lys Asn Trp Arg Leu Thr Asp Thr Glu Ile Arg Ile Leu			
250	255	260	
ggt gca ttt ttt gga aag aac cct ctg aaa aac ttc cag cag ttg aat			1110
Gly Ala Phe Phe Gly Lys Asn Pro Leu Lys Asn Phe Gln Gln Leu Asn			
265	270	275	
ttg gcg gga aat cgt gtg agc agt gat gga tgg ctt gcc ttc atg ggt			1158
Leu Ala Gly Asn Arg Val Ser Ser Asp Gly Trp Leu Ala Phe Met Gly			
280	285	290	
gta ttt gag aat ctt aag caa tta gtg ttt ttt gac ttt agt act aaa			1206
Val Phe Glu Asn Leu Lys Gln Leu Val Phe Phe Asp Phe Ser Thr Lys			
295	300	305	310

```

gaa ttt cta cct gat cca gca tta gtc aga aaa ctt agc caa gtg tta 1254
Glu Phe Leu Pro Asp Pro Ala Leu Val Arg Lys Leu Ser Gln Val Leu
      315                      320                      325

tcc aag tta act ttt ctg caa gaa gct agg ctt gtt ggg tgg caa ttt 1302
Ser Lys Leu Thr Phe Leu Gln Glu Ala Arg Leu Val Gly Trp Gln Phe
      330                      335                      340

gat gat gat gat ctc agt gtt att aca ggt gct ttt aaa cta gta act 1350
Asp Asp Asp Asp Leu Ser Val Ile Thr Gly Ala Phe Lys Leu Val Thr
      345                      350                      355

gct taaataaagt gtactcgaag caaaaaaaaaa aaaaaaaaaa aa 1395
Ala

```

<210> 99  
 <211> 359  
 <212> PRT  
 <213> Homo sapien

```

<400> 99
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
 1          5          10          15
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val
      20          25          30
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
      35          40          45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
      50          55          60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
      65          70          75          80
Phe Gln Asp Leu Asn Gly Gln Ser Gly Leu Thr Asp Ser Leu Gly Asn
      85          90          95
Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met Asn Glu
      100         105         110
Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys Lys Met
      115         120         125
Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly Met Asp
      130         135         140
Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu Glu Ile
      145         150         155         160
Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile Leu Ala
      165         170         175
Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu Ser Glu
      180         185         190
Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu Ile Asp
      195         200         205
Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro Trp Gly
      210         215         220
Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu Glu Glu

```

225		230		235		240									
Val	Pro	Gln	Leu	Val	Lys	Leu	Gly	Leu	Lys	Asn	Trp	Arg	Leu	Thr	Asp
		245				250							255		
Thr	Glu	Ile	Arg	Ile	Leu	Gly	Ala	Phe	Phe	Gly	Lys	Asn	Pro	Leu	Lys
		260				265							270		
Asn	Phe	Gln	Gln	Leu	Asn	Leu	Ala	Gly	Asn	Arg	Val	Ser	Ser	Asp	Gly
		275				280							285		
Trp	Leu	Ala	Phe	Met	Gly	Val	Phe	Glu	Asn	Leu	Lys	Gln	Leu	Val	Phe
		290				295							300		
Phe	Asp	Phe	Ser	Thr	Lys	Glu	Phe	Leu	Pro	Asp	Pro	Ala	Leu	Val	Arg
305					310					315					320
Lys	Leu	Ser	Gln	Val	Leu	Ser	Lys	Leu	Thr	Phe	Leu	Gln	Glu	Ala	Arg
				325					330						335
Leu	Val	Gly	Trp	Gln	Phe	Asp	Asp	Asp	Asp	Leu	Ser	Val	Ile	Thr	Gly
		340						345							350
Ala	Phe	Lys	Leu	Val	Thr	Ala									
		355													

<210> 100  
 <211> 578  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> CDS  
 <222> (277) ... (552)

<400> 100  
 cgcccgaggca ggtgtttata ctccggaggg tgtccccgtg cgtcatcggt ggagtggacc 60  
 aaaactggtg atctgtttgc cctgtgtgac cttgccaga accctgctga ctgagagaac 120  
 acatctgctg gaagtcctct gggattcaag gtacagggaa tgaagagtag ttttacagaa 180  
 aaaagaggac aatattggga tcacctttga cttttccatt tggaaataat attttctatt 240  
 gtgttataga aagggtggaa gctttcatcc agaaca atg aat ttc ata aag gac 294  
 Met Asn Phe Ile Lys Asp  
 1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342  
 Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln  
 10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390  
 Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val  
 25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438  
 Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile  
 40 45 50

att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 486  
 Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu  
 55 60 65 70



aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534  
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly  
75 80 85

caa agt ctt tta aca gct tagaaagtac agtagacata ctggggg 578  
Gln Ser Leu Leu Thr Ala  
90

<210> 101  
<211> 92  
<212> PRT  
<213> Homo sapien

<400> 101  
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly  
1 5 10 15  
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val  
20 25 30  
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln  
35 40 45  
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu  
50 55 60  
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu  
65 70 75 80  
Phe Gln Asp Leu Asn Gly Gln Ser Leu Leu Thr Ala  
85 90

<210> 102  
<211> 768  
<212> DNA  
<213> Homo sapien

<220>  
<221> CDS  
<222> (277) ... (744)

<400> 102  
cgcccggggca ggtgtttata ctccggaggg tgtccccgtg cgtcatcggt ggagtggacc 60  
aaaactggtg atctgtttgc cctgtgtgac cttgcccaga accctgctga ctgagagaac 120  
acatctgctg gaagtcctct gggattcaag gtacagggaa tgaagagtag ttttacagaa 180  
aaaagaggac aatattggga tcacctttga cttttccatt tggaaataat attttctatt 240  
gtgttataga aaggtgggaa gctttcatcc agaaca atg aat ttc ata aag gac 294  
Met Asn Phe Ile Lys Asp  
1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342  
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln  
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390  
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val

25	30	35	
aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc			438
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile			
40	45	50	
att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt			486
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu			
55	60	65	70
aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga			534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly			
75	80	85	
caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct			582
Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala			
90	95	100	
cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat			630
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr			
105	110	115	
ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc			678
Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys Ser Thr Phe			
120	125	130	
aca gaa cct gtc ctg tgg agg aag gac caa cac cat cac cgc gtg gag			726
Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His His Arg Val Glu			
135	140	145	150
cag ctg acc cta gtt tta tagcatcttc tacctgcccg ggcg			768
Gln Leu Thr Leu Val Leu			
155			

<210> 103  
 <211> 156  
 <212> PRT  
 <213> Homo sapien

<400> 103  
 Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly  
 1 5 10 15  
 Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val  
 20 25 30  
 Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln  
 35 40 45  
 Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu  
 50 55 60  
 Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu  
 65 70 75 80  
 Phe Gln Asp Leu Asn Gly Gln Ser Leu Phe His Gln Thr Ser Glu Gly  
 85 90 95

Asp	Leu	Asp	Asp	Leu	Ala	Gln	Asp	Leu	Lys	Asp	Leu	Tyr	His	Thr	Pro
		100						105					110		
Ser	Phe	Leu	Asn	Phe	Tyr	Pro	Leu	Gly	Glu	Asp	Ile	Asp	Ile	Ile	Phe
		115					120					125			
Asn	Leu	Lys	Ser	Thr	Phe	Thr	Glu	Pro	Val	Leu	Trp	Arg	Lys	Asp	Gln
		130				135					140				
His	His	His	Arg	Val	Glu	Gln	Leu	Thr	Leu	Val	Leu				
145					150					155					

<210> 104  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 104  
 aagaagagac ggctgcttat caat

24

<210> 105  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 105  
 ccacagcagg cctcgaagat gatc

24

<210> 106  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 106  
 atgatactcc tgaagaagag

20

<210> 107  
 <211> 1009  
 <212> PRT  
 <213> Homo sapien

Cys	Glu	Met	Cys	Ser	Gln	Glu	Ala	Phe	Gln	Ala	Gln	Arg	Ser	Gln	Leu
1			5					10					15		
Val	Glu	Leu	Leu	Val	Ser	Gly	Ser	Leu	Glu	Gly	Phe	Glu	Ser	Val	Leu
		20					25					30			

Asp	Trp	Leu	Leu	Ser	Trp	Glu	Val	Leu	Ser	Trp	Glu	Asp	Tyr	Glu	Gly
		35					40					45			
Phe	His	Leu	Leu	Gly	Gln	Pro	Leu	Ser	His	Leu	Ala	Arg	Arg	Leu	Leu
	50					55					60				
Asp	Thr	Val	Trp	Asn	Lys	Gly	Thr	Trp	Ala	Cys	Gln	Lys	Leu	Ile	Ala
65					70					75					80
Ala	Ala	Gln	Glu	Ala	Gln	Ala	Asp	Ser	Gln	Ser	Pro	Lys	Leu	His	Gly
				85					90					95	
Cys	Trp	Asp	Pro	His	Ser	Leu	His	Pro	Ala	Arg	Asp	Leu	Gln	Ser	His
			100					105					110		
Arg	Pro	Ala	Ile	Val	Arg	Arg	Leu	His	Ser	His	Val	Glu	Asn	Met	Leu
		115					120					125			
Asp	Leu	Ala	Trp	Glu	Arg	Gly	Phe	Val	Ser	Gln	Tyr	Glu	Cys	Asp	Glu
	130					135					140				
Ile	Arg	Leu	Pro	Ile	Phe	Thr	Pro	Ser	Gln	Arg	Ala	Arg	Arg	Leu	Leu
145					150					155					160
Asp	Leu	Ala	Thr	Val	Lys	Ala	Asn	Gly	Leu	Ala	Ala	Phe	Leu	Leu	Gln
				165					170					175	
His	Val	Gln	Glu	Leu	Pro	Val	Pro	Leu	Ala	Leu	Pro	Leu	Glu	Ala	Ala
			180					185					190		
Thr	Cys	Lys	Lys	Tyr	Met	Ala	Lys	Leu	Arg	Thr	Thr	Val	Ser	Ala	Gln
		195					200					205			
Ser	Arg	Phe	Leu	Ser	Thr	Tyr	Asp	Gly	Ala	Glu	Thr	Leu	Cys	Leu	Glu
	210					215					220				
Asp	Ile	Tyr	Thr	Glu	Asn	Val	Leu	Glu	Val	Trp	Ala	Asp	Val	Gly	Met
225					230					235					240
Ala	Gly	Pro	Pro	Gln	Lys	Ser	Pro	Ala	Thr	Leu	Gly	Leu	Glu	Glu	Leu
				245					250					255	
Phe	Ser	Thr	Pro	Gly	His	Leu	Asn	Asp	Asp	Ala	Asp	Thr	Val	Leu	Val
			260					265					270		
Val	Gly	Glu	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Gln	Arg	Leu	His
		275					280					285			
Leu	Leu	Trp	Ala	Ala	Gly	Gln	Asp	Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe
	290					295					300				
Pro	Phe	Ser	Cys	Arg	Gln	Leu	Gln	Cys	Met	Ala	Lys	Pro	Leu	Ser	Val
305					310					315					320
Arg	Thr	Leu	Leu	Phe	Glu	His	Cys	Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu
				325					330					335	
Asp	Ile	Phe	Gln	Leu	Leu	Leu	Asp	His	Pro	Asp	Arg	Val	Leu	Leu	Thr
			340					345					350		
Phe	Asp	Gly	Phe	Asp	Glu	Phe	Lys	Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg
	355						360					365			
His	Cys	Ser	Pro	Thr	Asp	Pro	Thr	Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn
	370					375					380				
Leu															

450					455					460							
Trp	Met	Val	Ser	Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly		
465					470					475						480	
Ser	Pro	Lys	Thr	Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe		
485					490					495							
Leu	Leu	His	Ala	Thr	Pro	Pro	Asp	Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro		
500					505					510							
Ser	Leu	Leu	Arg	Gly	Arg	Leu	Pro	Thr	Leu	Leu	His	Leu	Gly	Arg	Leu		
515					520					525							
Ala	Leu	Trp	Gly	Leu	Gly	Met	Cys	Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln		
530					535					540							
Leu	Gln	Ala	Ala	Gln	Val	Ser	Pro	Asp	Asp	Ile	Ser	Leu	Gly	Phe	Leu		
545					550					555						560	
Val	Arg	Ala	Lys	Gly	Val	Val	Pro	Gly	Ser	Thr	Ala	Pro	Leu	Glu	Phe		
565					570					575							
Leu	His	Ile	Thr	Phe	Gln	Cys	Phe	Phe	Ala	Ala	Phe	Tyr	Leu	Ala	Leu		
580					585					590							
Ser	Ala	Asp	Val	Pro	Pro	Ala	Leu	Leu	Arg	His	Leu	Phe	Asn	Cys	Gly		
595					600					605							
Arg	Pro	Gly	Asn	Ser	Pro	Met	Ala	Arg	Leu	Leu	Pro	Thr	Met	Cys	Ile		
610					615					620							
Gln	Ala	Ser	Glu	Gly	Lys	Asp	Ser	Ser	Val	Ala	Ala	Leu	Leu	Gln	Lys		
625					630					635						640	
Ala	Glu	Pro	His	Asn	Leu	Gln	Ile	Thr	Ala	Ala	Phe	Leu	Ala	Gly	Leu		
645					650					655							
Leu	Ser	Arg	Glu	His	Trp	Gly	Leu	Leu	Ala	Glu	Cys	Gln	Thr	Ser	Glu		
660					665					670							
Lys	Ala	Leu	Leu	Arg	Arg	Gln	Ala	Cys	Ala	Arg	Trp	Cys	Leu	Ala	Arg		
675					680					685							
Ser	Leu	Arg	Lys	His	Phe	His	Ser	Ile	Pro	Pro	Ala	Ala	Pro	Gly	Glu		
690					695					700							
Ala	Lys	Ser	Val	His	Ala	Met	Pro	Gly	Phe	Ile	Trp	Leu	Ile	Arg	Ser		
705					710					715						720	
Leu	Tyr	Glu	Met	Gln	Glu	Glu	Arg	Leu	Ala	Arg	Lys	Ala	Ala	Arg	Gly		
725					730					735							
Leu	Asn	Val	Gly	His	Leu	Lys	Leu	Thr	Phe	Cys	Ser	Val	Gly	Pro	Thr		
740					745					750							
Glu	Cys	Ala	Ala	Leu	Ala	Phe	Val	Leu	Gln	His	Leu	Arg	Arg	Pro	Val		
755					760					765							
Ala	Leu	Gln	Leu	Asp	Tyr	Asn	Ser	Val	Gly	Asp	Ile	Gly	Val	Glu	Gln		
770					775					780							
Leu	Leu	Pro	Cys	Leu	Gly	Val	Cys	Lys	Ala	Leu	Tyr	Leu	Arg	Asp	Asn		
785					790					795						800	
Asn	Ile	Ser	Asp	Arg	Gly	Ile	Cys	Lys	Leu	Ile	Glu	Cys	Ala	Leu	His		
805					810					815							
Cys	Glu	Gln	Leu	Gln	Lys	Leu	Ala	Leu	Gly	Asn	Asn	Tyr	Ile	Thr	Ala		
820					825					830							
Ala	Gly	Ala	Gln	Val	Leu	Ala	Glu	Gly	Leu	Arg	Gly	Asn	Thr	Ser	Leu		
835					840					845							
Gln	Phe	Leu	Gly	Phe	Trp	Gly	Asn	Arg	Val	Gly	Asp	Glu	Gly	Ala	Gln		
850					855					860							
Ala	Leu	Ala	Glu	Ala	Leu	Gly	Asp	His	Gln	Ser	Leu	Arg	Trp	Leu	Ser		
865					870					875						880	

Leu	Val	Gly	Asn	Asn	Ile	Gly	Ser	Val	Gly	Ala	Gln	Ala	Leu	Ala	Leu
				885					890					895	
Met	Leu	Ala	Lys	Asn	Val	Met	Leu	Glu	Glu	Leu	Cys	Leu	Glu	Glu	Asn
			900					905					910		
His	Leu	Gln	Asp	Glu	Gly	Val	Cys	Ser	Leu	Ala	Glu	Gly	Leu	Lys	Lys
		915					920					925			
Asn	Ser	Ser	Leu	Lys	Ile	Leu	Asn	Ile	Lys	Ile	His	Ala	Ser	Gly	Phe
		930				935					940				
Asn	Lys	Leu	Leu	Glu	Ser	Ile	Phe	Cys	Ile	Leu	Leu	Val	Val	Glu	Ala
945					950				955					960	
Phe	Phe	Leu	Gln	Lys	Val	Val	Lys	Ile	Leu	Glu	Glu	Met	Val	Val	Ser
			965						970					975	
Trp	Leu	Glu	Val	Arg	Leu	Ser	Asn	Asn	Cys	Ile	Thr	Tyr	Leu	Gly	Ala
		980					985						990		
Glu	Ala	Leu	Leu	Gln	Ala	Leu	Glu	Arg	Asn	Asp	Thr	Ile	Leu	Glu	Val
		995					1000					1005			
Trp															

<210> 108

<400> 108  
000

<210> 109

<400> 109  
000

<210> 110

<400> 110  
000

<210> 111

<400> 111  
000

<210> 112

<400> 112  
000

<210> 113

<400> 113  
000

<210> 114

<400> 114

000

<210> 115

<400> 115  
000

<210> 116

<400> 116  
000

<210> 117

<400> 117  
000

<210> 118

<400> 118  
000

<210> 119

<400> 119  
000

<210> 120

<400> 120  
000

<210> 121

<400> 121  
000

<210> 122

<400> 122  
000

<210> 123

<400> 123  
000

<210> 124

<400> 124  
000

<210> 125

<400> 125  
000

<210> 126

<400> 126  
000

<210> 127

<400> 127  
000

<210> 128

<400> 128  
000

<210> 129

<400> 129  
000

<210> 130

<400> 130  
000

<210> 131

<400> 131  
000

<210> 132

<400> 132  
000

<210> 133

<400> 133  
000

<210> 134

<400> 134  
000

<210> 135

<400> 135  
000



<210> 136

<400> 136  
000

<210> 137

<400> 137  
000

<210> 138

<400> 138  
000

<210> 139

<400> 139  
000

<210> 140

<400> 140  
000

<210> 141

<400> 141  
000

<210> 142

<400> 142  
000

<210> 143

<400> 143  
000

<210> 144

<400> 144  
000

<210> 145

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 145  
ccagaattca tggccgacaa ggtcctgaag 30

<210> 146  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 146  
ccactcgagc taatttccag gtatcggacc 30

<210> 147  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 147  
gaagacagtt acctggcaga 20

<210> 148  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 148  
ttgtattctg aacatggcac c 21

<210> 149  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 149  
gatcatcatc caggccgccc gtggtgacag ccctgg 36

<210> 150  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 150

ccagggtgt caccacgggc ggcctggatg atgac 36

<210> 151

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 151

cggaattcat ggccgacaag gtcctg 26

<210> 152

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 152

cgctcgagtt agtcttgcatttccaga 38

<210> 153

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 153

catgtgaatg atccctctag cag 23

<210> 154

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 154

gggctcggct atcgtgctct a 21

<210> 155

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 155

acgatagccg agcccttatt c

21

<210> 156

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 156

gtatggaatg ttctgaatcg c

21

<210> 157

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 157

cccggatcca tgaatttcatt aaaggacaat agc

33

<210> 158

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 158

cccttcgaac aagtcctgaa atagaggata

30

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 159

ggtggagcag gatgctgcta gagg

24

<210> 160

<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 160  
cacagtgggc caggctccga atgaagtca 29

<210> 161  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 161  
catcatttgc tgcgagaagg tggag 25

<210> 162  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 162  
ttaacttgga taacacttgg ctaag 25

<210> 163  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 163  
gtaaacatca ttgctgcga gaa 23

<210> 164  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 164  
cccgggcagg tagaagatgc tat 23

<210> 165  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 165  
aatttcataa aggacaatag ccgag 25

<210> 166  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 166  
tgtctactgt acttttctaag ctggt 25

<210> 167  
<211> 225  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(225)

<400> 167  
gag agt act ccc tca gag atc ata gaa aga gaa aga aaa aag ttg ctt 48  
Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys Lys Leu Leu  
1 5 10 15  
gaa atc ctt caa cat gat cct gat tct atc tta gac acg tta act tct 96  
Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser  
20 25 30  
cgg agg ctg att tct gag gaa gag tat gag act ctg gag aat gtt aca 144  
Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr  
35 40 45  
gat ctc ctg aag aaa agt cgg aag ctg tta att ttg gta cag aaa aag 192  
Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys  
50 55 60  
gga gag gcg acc tgt cag cat ttt ctc aag tgt 225  
Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys  
65 70 75

<210> 168  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens

<400> 168  
 Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys Lys Leu Leu  
 1 5 10 15  
 Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser  
 20 25 30  
 Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr  
 35 40 45  
 Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys  
 50 55 60  
 Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys  
 65 70 75

<210> 169  
 <211> 228  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(228)

<400> 169  
 atg tgc tcg cag gag gct ttt cag gca cag agg agc cag ctg gtc gag 48  
 Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu  
 1 5 10 15  
 ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg gac tgg 96  
 Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp  
 20 25 30  
 ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc ttc cac 144  
 Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His  
 35 40 45  
 ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg gac acc 192  
 Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr  
 50 55 60  
 gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc 228  
 Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu  
 65 70 75

<210> 170  
 <211> 76  
 <212> PRT

<213> Homo sapiens

<400> 170

Met	Cys	Ser	Gln	Glu	Ala	Phe	Gln	Ala	Gln	Arg	Ser	Gln	Leu	Val	Glu
1				5				10					15		
Leu	Leu	Val	Ser	Gly	Ser	Leu	Glu	Gly	Phe	Glu	Ser	Val	Leu	Asp	Trp
			20					25					30		
Leu	Leu	Ser	Trp	Glu	Val	Leu	Ser	Trp	Glu	Asp	Tyr	Glu	Gly	Phe	His
		35					40					45			
Leu	Leu	Gly	Gln	Pro	Leu	Ser	His	Leu	Ala	Arg	Arg	Leu	Leu	Asp	Thr
	50					55				60					
Val	Trp	Asn	Lys	Gly	Thr	Trp	Ala	Cys	Gln	Lys	Leu				
65					70					75					

<210> 171

<211> 243

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(243)

<400> 171

cca	gcc	cga	gac	ctg	cag	agt	cac	cgg	cca	gcc	att	gtc	agg	agg	ctc	48
Pro	Ala	Arg	Asp	Leu	Gln	Ser	His	Arg	Pro	Ala	Ile	Val	Arg	Arg	Leu	
1				5				10					15			
cac	agc	cat	gtg	gag	aac	atg	ctg	gac	ctg	gca	tgg	gag	cgg	ggg	ttc	96
His	Ser	His	Val	Glu	Asn	Met	Leu	Asp	Leu	Ala	Trp	Glu	Arg	Gly	Phe	
			20					25					30			
gtc	agc	cag	tat	gaa	tgt	gat	gaa	atc	agg	ttg	ccg	atc	ttc	aca	ccg	144
Val	Ser	Gln	Tyr	Glu	Cys	Asp	Glu	Ile	Arg	Leu	Pro	Ile	Phe	Thr	Pro	
		35					40					45				
tcc	cag	agg	gca	aga	agg	ctg	ctt	gat	ctt	gcc	acg	gtg	aaa	gcg	aat	192
Ser	Gln	Arg	Ala	Arg	Arg	Leu	Leu	Asp	Leu	Ala	Thr	Val	Lys	Ala	Asn	
	50					55				60						
gga	ttg	gct	gcc	ttc	ctt	cta	caa	cat	gtt	cag	gaa	tta	cca	gtc	cca	240
Gly	Leu	Ala	Ala	Phe	Leu	Leu	Gln	His	Val	Gln	Glu	Leu	Pro	Val	Pro	
65					70					75				80		
ttg																243
Leu																

<210> 172

<211> 81

<212> PRT



<213> Homo sapiens

<400> 172

Pro	Ala	Arg	Asp	Leu	Gln	Ser	His	Arg	Pro	Ala	Ile	Val	Arg	Arg	Leu
1				5					10					15	
His	Ser	His	Val	Glu	Asn	Met	Leu	Asp	Leu	Ala	Trp	Glu	Arg	Gly	Phe
			20					25					30		
Val	Ser	Gln	Tyr	Glu	Cys	Asp	Glu	Ile	Arg	Leu	Pro	Ile	Phe	Thr	Pro
		35					40					45			
Ser	Gln	Arg	Ala	Arg	Arg	Leu	Leu	Asp	Leu	Ala	Thr	Val	Lys	Ala	Asn
	50					55				60					
Gly	Leu	Ala	Ala	Phe	Leu	Leu	Gln	His	Val	Gln	Glu	Leu	Pro	Val	Pro
65					70					75					80
Leu															

<210> 173

<211> 888

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(888)

<400> 173

gac	gat	gcg	gac	act	gtg	ctg	gtg	gtg	ggt	gag	gcg	ggc	agt	ggc	aag	48
Asp	Asp	Ala	Asp	Thr	Val	Leu	Val	Val	Gly	Glu	Ala	Gly	Ser	Gly	Lys	
1				5					10					15		
agc	acg	ctc	ctg	cag	cgg	ctg	cac	ttg	ctg	tgg	gct	gca	ggg	caa	gac	96
Ser	Thr	Leu	Leu	Gln	Arg	Leu	His	Leu	Leu	Trp	Ala	Ala	Gly	Gln	Asp	
		20					25					30				
ttc	cag	gaa	ttt	ctc	ttt	gtc	ttc	cca	ttc	agc	tgc	cgg	cag	ctg	cag	144
Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe	Pro	Phe	Ser	Cys	Arg	Gln	Leu	Gln	
		35					40					45				
tgc	atg	gcc	aaa	cca	ctc	tct	gtg	cgg	act	cta	ctc	ttt	gag	cac	tgc	192
Cys	Met	Ala	Lys	Pro	Leu	Ser	Val	Arg	Thr	Leu	Leu	Phe	Glu	His	Cys	
	50					55				60						
tgt	tgg	cct	gat	gtt	ggc	caa	gaa	gac	atc	ttc	cag	tta	ctc	ctt	gac	240
Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu	Asp	Ile	Phe	Gln	Leu	Leu	Leu	Asp	
65				70					75						80	
cac	cct	gac	cgt	gtc	ctg	tta	acc	ttt	gat	ggc	ttt	gac	gag	ttc	aag	288
His	Pro	Asp	Arg	Val	Leu	Leu	Thr	Phe	Asp	Gly	Phe	Asp	Glu	Phe	Lys	
			85					90						95		
ttc	agg	ttc	acg	gat	cgt	gaa	cgc	cac	tgc	tcc	ccg	acc	gac	ccc	acc	336
Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg	His	Cys	Ser	Pro	Thr	Asp	Pro	Thr	

100	105	110	
tct gtc cag acc ctg ctc ttc aac ctt ctg cag ggc aac ctg ctg aag			384
Ser Val Gln Thr Leu Leu Phe Asn Leu Leu Gln Gly Asn Leu Leu Lys			
115	120	125	
aat gcc cgc aag gtg gtg acc agc cgt ccg gcc gct gtg tcg gcg ttc			432
Asn Ala Arg Lys Val Val Thr Ser Arg Pro Ala Ala Val Ser Ala Phe			
130	135	140	
ctc agg aag tac atc cgc acc gag ttc aac ctc aag ggc ttc tct gaa			480
Leu Arg Lys Tyr Ile Arg Thr Glu Phe Asn Leu Lys Gly Phe Ser Glu			
145	150	155	160
cag ggc atc gag ctg tac ctg agg aag cgc cat cat gag ccc ggg gtg			528
Gln Gly Ile Glu Leu Tyr Leu Arg Lys Arg His His Glu Pro Gly Val			
165	170	175	
gcg gac cgc ctc atc cgc ctg ctc caa gag acc tca gcc ctg cac ggt			576
Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser Ala Leu His Gly			
180	185	190	
ttg tgc cac ctg cct gtc ttc tca tgg atg gtg tcc aaa tgc cac cag			624
Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser Lys Cys His Gln			
195	200	205	
gaa ctg ttg ctg cag gag ggg ggg tcc cca aag acc act aca gat atg			672
Glu Leu Leu Leu Gln Glu Gly Gly Ser Pro Lys Thr Thr Thr Asp Met			
210	215	220	
tac ctg ctg att ctg cag cat ttt ctg ctg cat gcc acc ccc cca gac			720
Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala Thr Pro Pro Asp			
225	230	235	240
tca gct tcc caa ggt ctg gga ccc agt ctt ctt cgg ggc cgc ctc ccc			768
Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg Gly Arg Leu Pro			
245	250	255	
acc ctc ctg cac ctg ggc aga ctg gct ctg tgg ggc ctg ggc atg tgc			816
Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly Leu Gly Met Cys			
260	265	270	
tgc tac gtg ttc tca gcc cag cag ctc cag gca gca cag gtc agc cct			864
Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala Gln Val Ser Pro			
275	280	285	
gat gac att tct ctt ggc ttc ctg			888
Asp Asp Ile Ser Leu Gly Phe Leu			
290	295		

<210> 174

<211> 296

<212> PRT

<213> Homo sapiens

<400> 174

Asp	Asp	Ala	Asp	Thr	Val	Leu	Val	Val	Gly	Glu	Ala	Gly	Ser	Gly	Lys
1				5					10					15	
Ser	Thr	Leu	Leu	Gln	Arg	Leu	His	Leu	Leu	Trp	Ala	Ala	Gly	Gln	Asp
		20						25					30		
Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe	Pro	Phe	Ser	Cys	Arg	Gln	Leu	Gln
		35					40					45			
Cys	Met	Ala	Lys	Pro	Leu	Ser	Val	Arg	Thr	Leu	Leu	Phe	Glu	His	Cys
	50					55				60					
Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu	Asp	Ile	Phe	Gln	Leu	Leu	Leu	Asp
65				70					75					80	
His	Pro	Asp	Arg	Val	Leu	Leu	Thr	Phe	Asp	Gly	Phe	Asp	Glu	Phe	Lys
			85					90						95	
Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg	His	Cys	Ser	Pro	Thr	Asp	Pro	Thr
			100					105					110		
Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn	Leu	Leu	Gln	Gly	Asn	Leu	Leu	Lys
		115					120					125			
Asn	Ala	Arg	Lys	Val	Val	Thr	Ser	Arg	Pro	Ala	Ala	Val	Ser	Ala	Phe
	130					135				140					
Leu	Arg	Lys	Tyr	Ile	Arg	Thr	Glu	Phe	Asn	Leu	Lys	Gly	Phe	Ser	Glu
145				150					155						160
Gln	Gly	Ile	Glu	Leu	Tyr	Leu	Arg	Lys	Arg	His	His	Glu	Pro	Gly	Val
			165					170						175	
Ala	Asp	Arg	Leu	Ile	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Ala	Leu	His	Gly
			180					185					190		
Leu	Cys	His	Leu	Pro	Val	Phe	Ser	Trp	Met	Val	Ser	Lys	Cys	His	Gln
	195						200					205			
Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly	Ser	Pro	Lys	Thr	Thr	Thr	Asp	Met
	210					215					220				
Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe	Leu	Leu	His	Ala	Thr	Pro	Pro	Asp
225				230						235					240
Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro	Ser	Leu	Leu	Arg	Gly	Arg	Leu	Pro
			245					250						255	
Thr	Leu	Leu	His	Leu	Gly	Arg	Leu	Ala	Leu	Trp	Gly	Leu	Gly	Met	Cys
			260				265						270		
Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln	Leu	Gln	Ala	Ala	Gln	Val	Ser	Pro
		275				280						285			
Asp	Asp	Ile	Ser	Leu	Gly	Phe	Leu								
	290					295									

<210> 175

<211> 1209

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1209)

<400> 175

gag ccc ggg gtg gcg gac cgc ctc atc cgc ctg ctc caa gag acc tca	48
Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser	
1 5 10 15	
gcc ctg cac ggt ttg tgc cac ctg cct gtc ttc tca tgg atg gtg tcc	96
Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser	
20 25 30	
aaa tgc cac cag gaa ctg ttg ctg cag gag ggg ggg tcc cca aag acc	144
Lys Cys His Gln Glu Leu Leu Leu Gln Glu Gly Gly Ser Pro Lys Thr	
35 40 45	
act aca gat atg tac ctg ctg att ctg cag cat ttt ctg ctg cat gcc	192
Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala	
50 55 60	
acc ccc cca gac tca gct tcc caa ggt ctg gga ccc agt ctt ctt cgg	240
Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg	
65 70 75 80	
ggc cgc ctc ccc acc ctc ctg cac ctg ggc aga ctg gct ctg tgg ggc	288
Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly	
85 90 95	
ctg ggc atg tgc tgc tac gtg ttc tca gcc cag cag ctc cag gca gca	336
Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala	
100 105 110	
cag gtc agc cct gat gac att tct ctt ggc ttc ctg gtg cgt gcc aaa	384
Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu Val Arg Ala Lys	
115 120 125	
ggc gtc gtg cca ggg agt acg gcg ccc ctg gaa ttc ctt cac atc act	432
Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe Leu His Ile Thr	
130 135 140	
ttc cag tgc ttc ttt gcc gcg ttc tac ctg gca ctc agt gct gat gtg	480
Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu Ser Ala Asp Val	
145 150 155 160	
cca cca gct ttg ctc aga cac ctc ttc aat tgt ggc agg cca ggc aac	528
Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly Arg Pro Gly Asn	
165 170 175	
tca cca atg gcc agg ctc ctg ccc acg atg tgc atc cag gcc tcg gag	576
Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile Gln Ala Ser Glu	
180 185 190	
gga aag gac agc agc gtg gca gct ttg ctg cag aag gcc gag ccg cac	624
Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys Ala Glu Pro His	
195 200 205	

aac ctt cag atc aca gca gcc ttc ctg gca ggg ctg ttg tcc cgg gag	672
Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu Leu Ser Arg Glu	
210 215 220	
 cac tgg ggc ctg ctg gct gag tgc cag aca tct gag aag gcc ctg ctc	720
His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu Lys Ala Leu Leu	
225 230 235 240	
 cgg cgc cag gcc tgt gcc cgc tgg tgt ctg gcc cgc agc ctc cgc aag	768
Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg Ser Leu Arg Lys	
245 250 255	
 cac ttc cac tcc atc ccg cca gct gca ccg ggt gag gcc aag agc gtg	816
His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu Ala Lys Ser Val	
260 265 270	
 cat gcc atg ccc ggg ttc atc tgg ctc atc cgg agc ctg tac gag atg	864
His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met	
275 280 285	
 cag gag gag cgg ctg gct cgg aag gct gca cgt ggc ctg aat gtt ggg	912
Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly Leu Asn Val Gly	
290 295 300	
 cac ctc aag ttg aca ttt tgc agt gtg ggc ccc act gag tgt gct gcc	960
His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr Glu Cys Ala Ala	
305 310 315 320	
 ctg gcc ttt gtg ctg cag cac ctc cgg cgg ccc gtg gcc ctg cag ctg	1008
Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val Ala Leu Gln Leu	
325 330 335	
 gac tac aac tct gtg ggt gac att ggc gtg gag cag ctg ctg cct tgc	1056
Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln Leu Leu Pro Cys	
340 345 350	
 ctt ggt gtc tgc aag gct ctg tat ttg cgc gat aac aat atc tca gac	1104
Leu Gly Val Cys Lys Ala Leu Tyr Leu Arg Asp Asn Asn Ile Ser Asp	
355 360 365	
 cga ggc atc tgc aag ctc att gaa tgt gct ctt cac tgc gag caa ttg	1152
Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His Cys Glu Gln Leu	
370 375 380	
 cag aag tta gcg ctg ggg aat aac tac atc act gcc gcg gga gcc caa	1200
Gln Lys Leu Ala Leu Gly Asn Asn Tyr Ile Thr Ala Ala Gly Ala Gln	
385 390 395 400	
 gtg ctg gcc	1209
Val Leu Ala	

<210> 176  
<211> 403  
<212> PRT  
<213> Homo sapiens

<400> 176

Glu	Pro	Gly	Val	Ala	Asp	Arg	Leu	Ile	Arg	Leu	Leu	Gln	Glu	Thr	Ser
1				5					10					15	
Ala	Leu	His	Gly	Leu	Cys	His	Leu	Pro	Val	Phe	Ser	Trp	Met	Val	Ser
			20					25					30		
Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly	Ser	Pro	Lys	Thr
		35					40					45			
Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe	Leu	Leu	His	Ala
	50					55					60				
Thr	Pro	Pro	Asp	Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro	Ser	Leu	Leu	Arg
65					70				75						80
Gly	Arg	Leu	Pro	Thr	Leu	Leu	His	Leu	Gly	Arg	Leu	Ala	Leu	Trp	Gly
				85					90					95	
Leu	Gly	Met	Cys	Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln	Leu	Gln	Ala	Ala
			100					105					110		
Gln	Val	Ser	Pro	Asp	Asp	Ile	Ser	Leu	Gly	Phe	Leu	Val	Arg	Ala	Lys
		115					120					125			
Gly	Val	Val	Pro	Gly	Ser	Thr	Ala	Pro	Leu	Glu	Phe	Leu	His	Ile	Thr
	130					135					140				
Phe	Gln	Cys	Phe	Phe	Ala	Ala	Phe	Tyr	Leu	Ala	Leu	Ser	Ala	Asp	Val
145					150				155						160
Pro	Pro	Ala	Leu	Leu	Arg	His	Leu	Phe	Asn	Cys	Gly	Arg	Pro	Gly	Asn
				165				170						175	
Ser	Pro	Met	Ala	Arg	Leu	Leu	Pro	Thr	Met	Cys	Ile	Gln	Ala	Ser	Glu
		180					185					190			
Gly	Lys	Asp	Ser	Ser	Val	Ala	Ala	Leu	Leu	Gln	Lys	Ala	Glu	Pro	His
	195					200						205			
Asn	Leu	Gln	Ile	Thr	Ala	Ala	Phe	Leu	Ala	Gly	Leu	Leu	Ser	Arg	Glu
	210				215					220					
His	Trp	Gly	Leu	Leu	Ala	Glu	Cys	Gln	Thr	Ser	Glu	Lys	Ala	Leu	Leu
225					230				235						240
Arg	Arg	Gln	Ala	Cys	Ala	Arg	Trp	Cys	Leu	Ala	Arg	Ser	Leu	Arg	Lys
			245					250						255	
His	Phe	His	Ser	Ile	Pro	Pro	Ala	Ala	Pro	Gly	Glu	Ala	Lys	Ser	Val
		260					265						270		
His	Ala	Met	Pro	Gly	Phe	Ile	Trp	Leu	Ile	Arg	Ser	Leu	Tyr	Glu	Met
	275					280					285				
Gln	Glu	Glu	Arg	Leu	Ala	Arg	Lys	Ala	Ala	Arg	Gly	Leu	Asn	Val	Gly
	290				295					300					
His	Leu	Lys	Leu	Thr	Phe	Cys	Ser	Val	Gly	Pro	Thr	Glu	Cys	Ala	Ala
305					310				315						320
Leu	Ala	Phe	Val	Leu	Gln	His	Leu	Arg	Arg	Pro	Val	Ala	Leu	Gln	Leu
			325					330						335	
Asp	Tyr	Asn	Ser	Val	Gly	Asp	Ile	Gly	Val	Glu	Gln	Leu	Leu	Pro	Cys
		340				345						350			
Leu	Gly	Val	Cys	Lys	Ala	Leu	Tyr	Leu	Arg	Asp	Asn	Asn	Ile	Ser	Asp
	355					360					365				
Arg	Gly	Ile	Cys	Lys	Leu	Ile	Glu	Cys	Ala	Leu	His	Cys	Glu	Gln	Leu

370	375	380
Gln Lys Leu Ala Leu Gly Asn Asn Tyr Ile Thr Ala Ala Gly Ala Gln		
385	390	395
Val Leu Ala		400

<210> 177  
 <211> 261  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (261)

<400> 177	
atg aat ttc ata aag gac aat agc cga gcc ctt att caa aga atg gga	48
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly	
1 5 10 15	
atg act gtt ata aag caa atc aca gat gac cta ttt gta tgg aat gtt	96
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val	
20 25 30	
ctg aat cgc gaa gaa gta aac atc att tgc tgc gag aag gtg gag cag	144
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln	
35 40 45	
gat gct gct aga ggg atc att cac atg att ttg aaa aag ggt tca gag	192
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu	
50 55 60	
tcc tgt aac ctc ttt ctt aaa tcc ctt aag gag tgg aac tat cct cta	240
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu	
65 70 75 80	
ttt cag gac ttg aat gga caa	261
Phe Gln Asp Leu Asn Gly Gln	
85	

<210> 178  
 <211> 87  
 <212> PRT  
 <213> Homo sapiens

<400> 178	
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly	
1 5 10 15	
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val	
20 25 30	
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln	

	35		40		45	
Asp	Ala	Ala	Arg	Gly	Ile	Ile
50					55	
Ser	Cys	Asn	Leu	Phe	Leu	Lys
65					70	
Phe	Gln	Asp	Leu	Asn	Gly	Gln
					85	

<210> 179  
 <211> 891  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(891)

<400> 179	
ctt cag agc ccc tgc atc att gaa ggg gaa tct ggc aaa ggc aag tcc	48
Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser	
1 5 10 15	
act ctg ctg cag cgc att gcc atg ctc tgg ggc tcc gga aag tgc aag	96
Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys	
20 25 30	
gct ctg acc aag ttc aaa ttc gtc ttc ttc ctc cgt ctc agc agg gcc	144
Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala	
35 40 45	
cag ggt gga ctt ttt gaa acc ctc tgt gat caa ctc ctg gat ata cct	192
Gln Gly Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro	
50 55 60	
ggc aca atc agg aag cag aca ttc atg gcc atg ctg ctg aag ctg cgg	240
Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg	
65 70 75 80	
cag agg gtt ctt ttc ctt ctt gat ggc tac aat gaa ttc aag ccc cag	288
Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln	
85 90 95	
aac tgc cca gaa atc gaa gcc ctg ata aag gaa aac cac cgc ttc aag	336
Asn Cys Pro Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys	
100 105 110	
aac atg gtc atc gtc acc act acc act gag tgc ctg agg cac ata cgg	384
Asn Met Val Ile Val Thr Thr Thr Thr Glu Cys Leu Arg His Ile Arg	
115 120 125	
cag ttt ggt gcc ctg act gct gag gtg ggg gat atg aca gaa gac agc	432
Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser	



130	135	140	
gcc cag gct ctc atc cga gaa gtg ctg atc aag gag ctt gct gaa ggc			480
Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly			
145	150	155	160
ttg ttg ctc caa att cag aaa tcc agg tgc ttg agg aat ctc atg aag			528
Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys			
	165	170	175
acc cct ctc ttt gtg gtc atc act tgt gca atc cag atg ggt gaa agt			576
Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser			
	180	185	190
gag ttc cac tct cac aca caa aca acg ctg ttc cat acc ttc tat gat			624
Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp			
	195	200	205
ctg ttg ata cag aaa aac aaa cac aaa cat aaa ggt gtg gct gca agt			672
Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser			
	210	215	220
gac ttc att cgg agc ctg gac cac cgt gga gac cta gct ctg gag ggt			720
Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly			
	225	230	235
gtg ttc tcc cac aag ttt gat ttc gaa ctg cag gat gtg tcc agc gtg			768
Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val			
	245	250	255
aat gag gat gtc ctg ctg aca act ggg ctc ctc tgt aaa tat aca gct			816
Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala			
	260	265	270
caa agg ttc aag cca aag tat aaa ttc ttt cac aag tca ttc cag gag			864
Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu			
	275	280	285
tac aca gca gga cga aga ctc agc agt			891
Tyr Thr Ala Gly Arg Arg Leu Ser Ser			
	290	295	

<210> 180  
 <211> 297  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
 Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser  
 1 5 10 15  
 Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys  
 20 25 30

Ala	Leu	Thr	Lys	Phe	Lys	Phe	Val	Phe	Phe	Leu	Arg	Leu	Ser	Arg	Ala
	35						40					45			
Gln	Gly	Gly	Leu	Phe	Glu	Thr	Leu	Cys	Asp	Gln	Leu	Leu	Asp	Ile	Pro
	50					55					60				
Gly	Thr	Ile	Arg	Lys	Gln	Thr	Phe	Met	Ala	Met	Leu	Leu	Lys	Leu	Arg
65					70				75					80	
Gln	Arg	Val	Leu	Phe	Leu	Leu	Asp	Gly	Tyr	Asn	Glu	Phe	Lys	Pro	Gln
				85				90						95	
Asn	Cys	Pro	Glu	Ile	Glu	Ala	Leu	Ile	Lys	Glu	Asn	His	Arg	Phe	Lys
			100					105					110		
Asn	Met	Val	Ile	Val	Thr	Thr	Thr	Thr	Glu	Cys	Leu	Arg	His	Ile	Arg
	115					120						125			
Gln	Phe	Gly	Ala	Leu	Thr	Ala	Glu	Val	Gly	Asp	Met	Thr	Glu	Asp	Ser
	130					135					140				
Ala	Gln	Ala	Leu	Ile	Arg	Glu	Val	Leu	Ile	Lys	Glu	Leu	Ala	Glu	Gly
145					150					155				160	
Leu	Leu	Leu	Gln	Ile	Gln	Lys	Ser	Arg	Cys	Leu	Arg	Asn	Leu	Met	Lys
			165					170						175	
Thr	Pro	Leu	Phe	Val	Val	Ile	Thr	Cys	Ala	Ile	Gln	Met	Gly	Glu	Ser
		180					185						190		
Glu	Phe	His	Ser	His	Thr	Gln	Thr	Thr	Leu	Phe	His	Thr	Phe	Tyr	Asp
	195					200						205			
Leu	Leu	Ile	Gln	Lys	Asn	Lys	His	Lys	His	Lys	Gly	Val	Ala	Ala	Ser
	210					215					220				
Asp	Phe	Ile	Arg	Ser	Leu	Asp	His	Arg	Gly	Asp	Leu	Ala	Leu	Glu	Gly
225					230					235				240	
Val	Phe	Ser	His	Lys	Phe	Asp	Phe	Glu	Leu	Gln	Asp	Val	Ser	Ser	Val
			245					250						255	
Asn	Glu	Asp	Val	Leu	Leu	Thr	Thr	Gly	Leu	Leu	Cys	Lys	Tyr	Thr	Ala
		260					265						270		
Gln	Arg	Phe	Lys	Pro	Lys	Tyr	Lys	Phe	Phe	His	Lys	Ser	Phe	Gln	Glu
	275					280						285			
Tyr	Thr	Ala	Gly	Arg	Arg	Leu	Ser	Ser							
	290					295									

<210> 181  
 <211> 618  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(618)

<400> 181																
ggt	aac	ttg	aag	aac	ctt	aca	aag	ctc	ata	atg	gat	aac	ata	aag	atg	48
Gly	Asn	Leu	Lys	Asn	Leu	Thr	Lys	Leu	Ile	Met	Asp	Asn	Ile	Lys	Met	
1				5				10						15		
aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg aag															96	
Asn	Glu	Glu	Asp	Ala	Ile	Lys	Leu	Ala	Glu	Gly	Leu	Lys	Asn	Leu	Lys	
		20						25					30			

aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag gga	144
Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly	
35 40 45	
atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt gaa	192
Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu	
50 55 60	
gaa att caa tta gtc tcc tgc tgc ttg tct gca aat gca gtg aaa atc	240
Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile	
65 70 75 80	
cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat tta	288
Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu	
85 90 95	
tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa ctg	336
Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu	
100 105 110	
atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg ccc	384
Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro	
115 120 125	
tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat ttg	432
Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu	
130 135 140	
gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga ctc	480
Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu	
145 150 155 160	
aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac cct	528
Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro	
165 170 175	
ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc agt	576
Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser	
180 185 190	
gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag	618
Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys	
195 200 205	

<210> 182  
 <211> 206  
 <212> PRT  
 <213> Homo sapiens

<400> 182

```

Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met
 1          5          10          15
Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys
          20          25          30
Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly
          35          40          45
Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu
          50          55          60
Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile
65          70          75          80
Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu
          85          90          95
Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu
          100          105          110
Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro
          115          120          125
Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu
          130          135          140
Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu
145          150          155          160
Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro
          165          170          175
Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser
          180          185          190
Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys
          195          200          205

```

<210> 183  
 <211> 165  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> '(1)...(165)

```

<400> 183
acc tac att ccc agc agg gct gta tct ttg ttc ttc aac tgg aag cag   48
Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln
 1          5          10          15

gaa ttc agg act ctg gag gtc aca ctc cgg gat ttc agc aag ttg aat   96
Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn
          20          25          30

aag caa gat atc aga tat ctg ggg aaa ata ttc agc tct gcc aca agc   144
Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser
          35          40          45

ctc agg ctg caa ata aag aga                                     165
Leu Arg Leu Gln Ile Lys Arg
          50          55

```

<210> 184  
 <211> 55  
 <212> PRT  
 <213> Homo sapiens

<400> 184  
 Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln  
 1 5 10 15  
 Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn  
 20 25 30  
 Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser  
 35 40 45  
 Leu Arg Leu Gln Ile Lys Arg  
 50 55

<210> 185  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 185  
 gaaatgtgct cgcaggagg 19

<210> 186  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 186  
 gatgagcttc tgacaggccc 20

<210> 187  
 <211> 3063  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (2385)

<221> CDS  
 <222> (2389) ... (2928)

<400> 187

tgt gaa atg tgc tcg cag gag gct ttt cag gca cag agg agc cag ctg	48
Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu	
1 5 10 15	
gtc gag ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg	96
Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu	
20 25 30	
gac tgg ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc	144
Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly	
35 40 45	
ttc cac ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg	192
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu	
50 55 60	
gac acc gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc atc gcg	240
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala	
65 70 75 80	
gct gcc caa gaa gcc cag gcc gac agc cag tcc ccc aag ctg cat ggc	288
Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly	
85 90 95	
tgc tgg gac ccc cac tcg ctc cac cca gcc cga gac ctg cag agt cac	336
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His	
100 105 110	
cgg cca gcc att gtc agg agg ctc cac agc cat gtg gag aac atg ctg	384
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu	
115 120 125	
gac ctg gca tgg gag cgg ggt ttc gtc agc cag tat gaa tgt gat gaa	432
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu	
130 135 140	
atc agg ttg ccg atc ttc aca ccg tcc cag agg gca aga agg ctg ctt	480
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu	
145 150 155 160	
gat ctt gcc acg gtg aaa gcg aat gga ttg gct gcc ttc ctt cta caa	528
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln	
165 170 175	
cat gtt cag gaa tta cca gtc cca ttg gcc ctg cct ttg gaa gct gcc	576
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala	
180 185 190	
aca tgc aag aag tat atg gcc aag ctg agg acc acg gtg tct gct cag	624
Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln	
195 200 205	
tct cgc ttc ctc agt acc tat gat gga gca gag acg ctc tgc ctg gag	672

Ser	Arg	Phe	Leu	Ser	Thr	Tyr	Asp	Gly	Ala	Glu	Thr	Leu	Cys	Leu	Glu		
210						215					220						
gac	ata	tac	aca	gag	aat	gtc	ctg	gag	gtc	tgg	gca	gat	gtg	ggc	atg	720	
Asp	Ile	Tyr	Thr	Glu	Asn	Val	Leu	Glu	Val	Trp	Ala	Asp	Val	Gly	Met		
225					230					235					240		
gct	gga	ccc	ccg	cag	aag	agc	cca	gcc	acc	ctg	ggc	ctg	gag	gag	ctc	768	
Ala	Gly	Pro	Pro	Gln	Lys	Ser	Pro	Ala	Thr	Leu	Gly	Leu	Glu	Glu	Leu		
				245					250					255			
ttc	agc	acc	cct	ggc	cac	ctc	aat	gac	gat	gcg	gac	act	gtg	ctg	gtg	816	
Phe	Ser	Thr	Pro	Gly	His	Leu	Asn	Asp	Asp	Ala	Asp	Thr	Val	Leu	Val		
			260					265					270				
gtg	ggt	gag	gcg	ggc	agt	ggc	aag	agc	acg	ctc	ctg	cag	cgg	ctg	cac	864	
Val	Gly	Glu	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Gln	Arg	Leu	His		
		275					280					285					
ttg	ctg	tgg	gct	gca	ggg	caa	gac	ttc	cag	gaa	ttt	ctc	ttt	gtc	ttc	912	
Leu	Leu	Trp	Ala	Ala	Gly	Gln	Asp	Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe		
		290				295					300						
cca	ttc	agc	tgc	cgg	cag	ctg	cag	tgc	atg	gcc	aaa	cca	ctc	tct	gtg	960	
Pro	Phe	Ser	Cys	Arg	Gln	Leu	Gln	Cys	Met	Ala	Lys	Pro	Leu	Ser	Val		
305					310					315					320		
cgg	act	cta	ctc	ttt	gag	cac	tgc	tgt	tgg	cct	gat	gtt	ggt	caa	gaa	1008	
Arg	Thr	Leu	Leu	Phe	Glu	His	Cys	Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu		
				325					330					335			
gac	atc	ttc	cag	tta	ctc	ctt	gac	cac	cct	gac	cgt	gtc	ctg	tta	acc	1056	
Asp	Ile	Phe	Gln	Leu	Leu	Leu	Asp	His	Pro	Asp	Arg	Val	Leu	Leu	Thr		
			340					345					350				
ttt	gat	ggc	ttt	gac	gag	ttc	aag	ttc	agg	ttc	acg	gat	cgt	gaa	cgc	1104	
Phe	Asp	Gly	Phe	Asp	Glu	Phe	Lys	Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg		
		355					360					365					
cac	tgc	tcc	ccg	acc	gac	ccc	acc	tct	gtc	cag	acc	ctg	ctc	ttc	aac	1152	
His	Cys	Ser	Pro	Thr	Asp	Pro	Thr	Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn		
		370				375					380						
ctt	ctg	cag	ggc	aac	ctg	ctg	aag	aat	gcc	cgc	aag	gtg	gtg	acc	agc	1200	
Leu	Leu	Gln	Gly	Asn	Leu	Leu	Lys	Asn	Ala	Arg	Lys	Val	Val	Thr	Ser		
385					390					395					400		
cgt	ccg	gcc	gct	gtg	tcg	gcg	ttc	ctc	agg	aag	tac	atc	cgc	acc	gag	1248	
Arg	Pro	Ala	Ala	Val	Ser	Ala	Phe	Leu	Arg	Lys	Tyr	Ile	Arg	Thr	Glu		
			405					410					415				
ttc	aac	ctc	aag	ggc	ttc	tct	gaa	cag	ggc	atc	gag	ctg	tac	ctg	agg	1296	
Phe	Asn	Leu	Lys	Gly	Phe	Ser	Glu	Gln	Gly	Ile	Glu	Leu	Tyr	Leu	Arg		

420	425	430	
aag cgc cat cat gag ccc ggg gtg gcg gac cgc ctc atc cgc ctg ctc			1344
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu			
435	440	445	
caa gag acc tca gcc ctg cac ggt ttg tgc cac ctg cct gtc ttc tca			1392
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser			
450	455	460	
tgg atg gtg tcc aaa tgc cac cag gaa ctg ttg ctg cag gag ggg ggg			1440
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Leu Gln Glu Gly Gly			
465	470	475	480
tcc cca aag acc act aca gat atg tac ctg ctg att ctg cag cat ttt			1488
Ser Pro Lys Thr Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe			
485	490	495	
ctg ctg cat gcc acc ccc cca gac tca gct tcc caa ggt ctg gga ccc			1536
Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro			
500	505	510	
agt ctt ctt cgg ggc cgc ctc ccc acc ctc ctg cac ctg ggc aga ctg			1584
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu			
515	520	525	
gct ctg tgg ggc ctg ggc atg tgc tgc tac gtg ttc tca gcc cag cag			1632
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln			
530	535	540	
ctc cag gca gca cag gtc agc cct gat gac att tct ctt ggc ttc ctg			1680
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu			
545	550	555	560
gtg cgt gcc aaa ggt gtc gtg cca ggg agt acg gcg ccc ctg gaa ttc			1728
Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe			
565	570	575	
ctt cac atc act ttc cag tgc ttc ttt gcc gcg ttc tac ctg gca ctc			1776
Leu His Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu			
580	585	590	
agt gct gat gtg cca cca gct ttg ctc aga cac ctc ttc aat tgt ggc			1824
Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly			
595	600	605	
agg cca ggc aac tca cca atg gcc agg ctc ctg ccc acg atg tgc atc			1872
Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile			
610	615	620	
cag gcc tcg gag gga aag gac agc agc gtg gca gct ttg ctg cag aag			1920
Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys			
625	630	635	640



gcc gag ccg cac aac ctt cag atc aca gca gcc ttc ctg gca ggg ctg	1968
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu	
645 650 655	
ttg tcc cgg gag cac tgg ggc ctg ctg gct gag tgc cag aca tct gag	2016
Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu	
660 665 670	
aag gcc ctg ctc cgg cgc cag gcc tgt gcc cgc tgg tgt ctg gcc cgc	2064
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg	
675 680 685	
agc ctc cgc aag cac ttc cac tcc atc ccg cca gct gca ccg ggt gag	2112
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu	
690 695 700	
gcc aag agc gtg cat gcc atg ccc ggg ttc atc tgg ctc atc cgg agc	2160
Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser	
705 710 715 720	
ctg tac gag atg cag gag gag cgg ctg gct cgg aag gct gca cgt ggc	2208
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly	
725 730 735	
ctg aat gtt ggg cac ctc aag ttg aca ttt tgc agt gtg ggc ccc act	2256
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr	
740 745 750	
gag tgt gct gcc ctg gcc ttt gtg ctg cag cac ctc cgg cgg ccc gtg	2304
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val	
755 760 765	
gcc ctg cag ctg gac tac aac tct gtg ggt gac att ggc gtg gag cag	2352
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln	
770 775 780	
ctg ctg cct tgc ctt ggt gtc tgc aag gct ctg taa ttc tgg ggc aac	2400
Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu Phe Trp Gly Asn	
785 790 795	
aga gtg ggt gac gag ggg gcc cag gcc ctg gct gaa gcc ttg ggt gat	2448
Arg Val Gly Asp Glu Gly Ala Gln Ala Leu Ala Glu Ala Leu Gly Asp	
800 805 810 815	
cac cag agc ttg agg tgg ctc agc ctg gtg ggg aac aac att ggc agt	2496
His Gln Ser Leu Arg Trp Leu Ser Leu Val Gly Asn Asn Ile Gly Ser	
820 825 830	
gtg ggt gcc caa gcc ttg gca ctg atg ctg gca aag aac gtc atg cta	2544
Val Gly Ala Gln Ala Leu Ala Leu Met Leu Ala Lys Asn Val Met Leu	
835 840 845	

gaa gaa ctc tgc ctg gag gag aac cat ctc cag gat gaa ggt gta tgt 2592  
 Glu Glu Leu Cys Leu Glu Glu Asn His Leu Gln Asp Glu Gly Val Cys  
           850                                  855                                  860

tct ctc gca gaa gga ctg aag aaa aat tca agt ttg aaa atc ctg aac 2640  
 Ser Leu Ala Glu Gly Leu Lys Lys Asn Ser Ser Leu Lys Ile Leu Asn  
           865                                  870                                  875

ata aaa att cat gct tcg gga ttc aac aaa ctc ttg gaa agc att ttc 2688  
 Ile Lys Ile His Ala Ser Gly Phe Asn Lys Leu Leu Glu Ser Ile Phe  
           880                                  885                                  890                                  895

tgc atc ctc ctg gtt gtg gaa gca ttt ttc ctg cag aaa gtt gtc aag 2736  
 Cys Ile Leu Leu Val Val Glu Ala Phe Phe Leu Gln Lys Val Val Lys  
                                   900                                  905                                  910

att ctt gaa gaa atg gta gtc agt tgg cta gag gtc agg ttg tcc aat 2784  
 Ile Leu Glu Glu Met Val Val Ser Trp Leu Glu Val Arg Leu Ser Asn  
                                   915                                  920                                  925

aac tgc atc acc tac cta ggg gca gaa gcc ctc ctg cag gcc ctt gaa 2832  
 Asn Cys Ile Thr Tyr Leu Gly Ala Glu Ala Leu Leu Gln Ala Leu Glu  
                                   930                                  935                                  940

agg aat gac acc atc ctg gaa gtc tgg ctc cga ggg aac act ttc tct 2880  
 Arg Asn Asp Thr Ile Leu Glu Val Trp Leu Arg Gly Asn Thr Phe Ser  
           945                                  950                                  955

cta gag gag gtt gac aag ctc ggc tgc agg gac acc aga ctc ttg ctt 2928  
 Leu Glu Glu Val Asp Lys Leu Gly Cys Arg Asp Thr Arg Leu Leu Leu  
           960                                  965                                  970                                  975

tgaagtctcc gggaggatgt tcgtctcagt ttgtttgtga gcaggctgtg agtttgggcc 2988  
 ccagaggctg ggtgacatgt gttggcagcc tcttcaaaat gagccctgtc ctgcctaagg 3048  
 ctgaacttgt tttct 3063

<210> 188  
 <211> 795  
 <212> PRT  
 <213> Homo sapiens

<400> 188  
 Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu  
   1                                  5                                  10                                  15  
 Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu  
                                   20                                  25                                  30  
 Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly  
                                   35                                  40                                  45  
 Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu  
           50                                  55                                  60  
 Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala  
   65                                  70                                  75                                  80  
 Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly

				85					90				95				
Cys	Trp	Asp	Pro	His	Ser	Leu	His	Pro	Ala	Arg	Asp	Leu	Gln	Ser	His		
			100					105					110				
Arg	Pro	Ala	Ile	Val	Arg	Arg	Leu	His	Ser	His	Val	Glu	Asn	Met	Leu		
		115					120					125					
Asp	Leu	Ala	Trp	Glu	Arg	Gly	Phe	Val	Ser	Gln	Tyr	Glu	Cys	Asp	Glu		
	130					135					140						
Ile	Arg	Leu	Pro	Ile	Phe	Thr	Pro	Ser	Gln	Arg	Ala	Arg	Arg	Leu	Leu		
145					150					155					160		
Asp	Leu	Ala	Thr	Val	Lys	Ala	Asn	Gly	Leu	Ala	Ala	Phe	Leu	Leu	Gln		
				165				170							175		
His	Val	Gln	Glu	Leu	Pro	Val	Pro	Leu	Ala	Leu	Pro	Leu	Glu	Ala	Ala		
			180					185					190				
Thr	Cys	Lys	Lys	Tyr	Met	Ala	Lys	Leu	Arg	Thr	Thr	Val	Ser	Ala	Gln		
	195						200					205					
Ser	Arg	Phe	Leu	Ser	Thr	Tyr	Asp	Gly	Ala	Glu	Thr	Leu	Cys	Leu	Glu		
	210					215					220						
Asp	Ile	Tyr	Thr	Glu	Asn	Val	Leu	Glu	Val	Trp	Ala	Asp	Val	Gly	Met		
225					230					235					240		
Ala	Gly	Pro	Pro	Gln	Lys	Ser	Pro	Ala	Thr	Leu	Gly	Leu	Glu	Glu	Leu		
				245				250							255		
Phe	Ser	Thr	Pro	Gly	His	Leu	Asn	Asp	Asp	Ala	Asp	Thr	Val	Leu	Val		
			260					265					270				
Val	Gly	Glu	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Gln	Arg	Leu	His		
	275					280						285					
Leu	Leu	Trp	Ala	Ala	Gly	Gln	Asp	Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe		
	290					295				300							
Pro	Phe	Ser	Cys	Arg	Gln	Leu	Gln	Cys	Met	Ala	Lys	Pro	Leu	Ser	Val		
305					310					315					320		
Arg	Thr	Leu	Leu	Phe	Glu	His	Cys	Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu		
				325					330						335		
Asp	Ile	Phe	Gln	Leu	Leu	Leu	Asp	His	Pro	Asp	Arg	Val	Leu	Leu	Thr		
		340						345					350				
Phe	Asp	Gly	Phe	Asp	Glu	Phe	Lys	Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg		
	355						360					365					
His	Cys	Ser	Pro	Thr	Asp	Pro	Thr	Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn		
	370					375						380					
Leu	Leu	Gln	Gly	Asn	Leu	Leu	Lys	Asn	Ala	Arg	Lys	Val	Val	Thr	Ser		
385					390					395					400		
Arg	Pro	Ala	Ala	Val	Ser	Ala	Phe	Leu	Arg	Lys	Tyr	Ile	Arg	Thr	Glu		
				405				410							415		
Phe	Asn	Leu	Lys	Gly	Phe	Ser	Glu	Gln	Gly	Ile	Glu	Leu	Tyr	Leu	Arg		
		420						425					430				
Lys	Arg	His	His	Glu	Pro	Gly	Val	Ala	Asp	Arg	Leu	Ile	Arg	Leu	Leu		
	435						440						445				
Gln	Glu	Thr	Ser	Ala	Leu	His	Gly	Leu	Cys	His	Leu	Pro	Val	Phe	Ser		
	450					455						460					
Trp	Met	Val	Ser	Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly		
465					470					475					480		
Ser	Pro	Lys	Thr	Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe		
				485				490							495		
Leu	Leu	His	Ala	Thr	Pro	Pro	Asp	Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro		
			500					505					510				

Ser	Leu	Leu	Arg	Gly	Arg	Leu	Pro	Thr	Leu	Leu	His	Leu	Gly	Arg	Leu
		515					520					525			
Ala	Leu	Trp	Gly	Leu	Gly	Met	Cys	Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln
		530				535					540				
Leu	Gln	Ala	Ala	Gln	Val	Ser	Pro	Asp	Asp	Ile	Ser	Leu	Gly	Phe	Leu
545					550					555					560
Val	Arg	Ala	Lys	Gly	Val	Val	Pro	Gly	Ser	Thr	Ala	Pro	Leu	Glu	Phe
				565					570					575	
Leu	His	Ile	Thr	Phe	Gln	Cys	Phe	Phe	Ala	Ala	Phe	Tyr	Leu	Ala	Leu
			580					585					590		
Ser	Ala	Asp	Val	Pro	Pro	Ala	Leu	Leu	Arg	His	Leu	Phe	Asn	Cys	Gly
		595					600					605			
Arg	Pro	Gly	Asn	Ser	Pro	Met	Ala	Arg	Leu	Leu	Pro	Thr	Met	Cys	Ile
		610				615					620				
Gln	Ala	Ser	Glu	Gly	Lys	Asp	Ser	Ser	Val	Ala	Ala	Leu	Leu	Gln	Lys
625					630					635					640
Ala	Glu	Pro	His	Asn	Leu	Gln	Ile	Thr	Ala	Ala	Phe	Leu	Ala	Gly	Leu
				645					650					655	
Leu	Ser	Arg	Glu	His	Trp	Gly	Leu	Leu	Ala	Glu	Cys	Gln	Thr	Ser	Glu
			660					665					670		
Lys	Ala	Leu	Leu	Arg	Arg	Gln	Ala	Cys	Ala	Arg	Trp	Cys	Leu	Ala	Arg
		675				680						685			
Ser	Leu	Arg	Lys	His	Phe	His	Ser	Ile	Pro	Pro	Ala	Ala	Pro	Gly	Glu
		690				695					700				
Ala	Lys	Ser	Val	His	Ala	Met	Pro	Gly	Phe	Ile	Trp	Leu	Ile	Arg	Ser
705					710					715					720
Leu	Tyr	Glu	Met	Gln	Glu	Glu	Arg	Leu	Ala	Arg	Lys	Ala	Ala	Arg	Gly
				725					730					735	
Leu	Asn	Val	Gly	His	Leu	Lys	Leu	Thr	Phe	Cys	Ser	Val	Gly	Pro	Thr
			740					745					750		
Glu	Cys	Ala	Ala	Leu	Ala	Phe	Val	Leu	Gln	His	Leu	Arg	Arg	Pro	Val
		755					760					765			
Ala	Leu	Gln	Leu	Asp	Tyr	Asn	Ser	Val	Gly	Asp	Ile	Gly	Val	Glu	Gln
		770				775					780				
Leu	Leu	Pro	Cys	Leu	Gly	Val	Cys	Lys	Ala	Leu					
785					790					795					

```
<210> 189  
<211> 180  
<212> PRT  
<213> Homo sapiens
```

<400> 189

Phe	Trp	Gly	Asn	Arg	Val	Gly	Asp	Glu	Gly	Ala	Gln	Ala	Leu	Ala	Glu
1				5					10					15	
Ala	Leu	Gly	Asp	His	Gln	Ser	Leu	Arg	Trp	Leu	Ser	Leu	Val	Gly	Asn
			20					25					30		
Asn	Ile	Gly	Ser	Val	Gly	Ala	Gln	Ala	Leu	Ala	Leu	Met	Leu	Ala	Lys
		35					40					45			
Asn	Val	Met	Leu	Glu	Glu	Leu	Cys	Leu	Glu	Glu	Asn	His	Leu	Gln	Asp
	50					55					60				
Glu	Gly	Val	Cys	Ser	Leu	Ala	Glu	Gly	Leu	Lys	Lys	Asn	Ser	Ser	Leu

65		70		75		80									
Lys	Ile	Leu	Asn	Ile	Lys	Ile	His	Ala	Ser	Gly	Phe	Asn	Lys	Leu	Leu
			85						90					95	
Glu	Ser	Ile	Phe	Cys	Ile	Leu	Leu	Val	Val	Glu	Ala	Phe	Phe	Leu	Gln
			100					105						110	
Lys	Val	Val	Lys	Ile	Leu	Glu	Glu	Met	Val	Val	Ser	Trp	Leu	Glu	Val
			115					120						125	
Arg	Leu	Ser	Asn	Asn	Cys	Ile	Thr	Tyr	Leu	Gly	Ala	Glu	Ala	Leu	Leu
			130					135						140	
Gln	Ala	Leu	Glu	Arg	Asn	Asp	Thr	Ile	Leu	Glu	Val	Trp	Leu	Arg	Gly
			145					150						155	
Asn	Thr	Phe	Ser	Leu	Glu	Glu	Val	Asp	Lys	Leu	Gly	Cys	Arg	Asp	Thr
				165						170				175	
Arg	Leu	Leu	Leu												
			180												

<210> 190  
 <211> 721  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (193)...(612)

<400> 190  
 cctgggggttc ctgcacatta ccttccgtgc ttttttgccg ctttctactt ggctgtcagt 60  
 gctgacacat cggtggcctc tctcaagcac cttttcagct gtggccggct gggcagctca 120  
 ctgctgggaa ggctgctgcc caacctgtgt atccagggtc ccagagtcaa gaagggcagc 180  
 gaagcagccc tg ctg cag aag gct gag cca cac aac ctg caa atc aca gca 231  
 Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala  
 1 5 10

gcc ttc cta gca ggt ctg ttg tcc cag cag cat cgg gac ctg ttg gct 279  
 Ala Phe Leu Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Leu Ala  
 15 20 25

gca tgc cag gtc tcc gag agg gta ctg ctc cag cgt cag gca cgt gcc 327  
 Ala Cys Gln Val Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala  
 30 35 40 45

cgc tcg tgt ctg gcc cac agc ctc cgc gag cac ttc cat tcc atc ccg 375  
 Arg Ser Cys Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro  
 50 55 60

cct gcc gtg ccc ggt gag acc aag agc atg cat gct atg ccg ggc ttc 423  
 Pro Ala Val Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe  
 65 70 75

att tgg ctc atc cgt agc ctg tac gag atg cag gag gag cag ttg gcc 471  
 Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala  
 80 85 90

cag gag gct gtc cgt cgc ttg gac atc ggg cac ctg aag ttg aca ttt 519  
Gln Glu Ala Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe  
95 100 105

tgc aga gtg ggc cct gca gag tgt gct gca ctg gcc ttt gta ctg caa 567  
Cys Arg Val Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln  
110 115 120 125

cat ctc cag cgg cct gtg gcc cta cag ctg gat tac aac tct gtg 612  
His Leu Gln Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser Val  
130 135 140

ggagatgttg ggagtggaac agctgcgacc gtgcctttgg ggtctgcaca gctctgtagt 672  
gagtgtgaca aggtcttgcc gattgggcct gtggcaaag ctactgtca 721

<210> 191  
<211> 140  
<212> PRT  
<213> Mus musculus

<400> 191  
Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu  
1 5 10 15  
Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Leu Ala Ala Cys Gln  
20 25 30  
Val Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala Arg Ser Cys  
35 40 45  
Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro Pro Ala Val  
50 55 60  
Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe Ile Trp Leu  
65 70 75 80  
Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala Gln Glu Ala  
85 90 95  
Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe Cys Arg Val  
100 105 110  
Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Gln  
115 120 125  
Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser Val  
130 135 140

<210> 192  
<211> 419  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (1)...(417)

<400> 192  
ctg cag aag gct gag cca cac aac ctg cag atc aca gca gcc ttc cta 48

Leu	Gln	Lys	Ala	Glu	Pro	His	Asn	Leu	Gln	Ile	Thr	Ala	Ala	Phe	Leu	
1				5					10					15		
gca	ggt	ctg	ttg	tcc	cag	cag	cat	cgg	gac	ctg	ttg	gct	gca	tgc	cag	96
Ala	Gly	Leu	Leu	Ser	Gln	Gln	His	Arg	Asp	Leu	Leu	Ala	Ala	Cys	Gln	
		20						25					30			
atc	tcc	gag	agg	gtg	ctg	ctc	cag	cgt	cag	gca	cgt	gcc	cgc	tcg	tgt	144
Ile	Ser	Glu	Arg	Val	Leu	Leu	Gln	Arg	Gln	Ala	Arg	Ala	Arg	Ser	Cys	
		35					40					45				
ctg	gcc	cac	agc	ctc	cgc	gag	cac	ttc	cat	tcc	atc	ccg	cct	gcc	gtg	192
Leu	Ala	His	Ser	Leu	Arg	Glu	His	Phe	His	Ser	Ile	Pro	Pro	Ala	Val	
	50					55				60						
ccc	ggt	gag	acc	aag	agc	atg	cat	gct	atg	ccg	ggc	ttt	att	tgg	ctc	240
Pro	Gly	Glu	Thr	Lys	Ser	Met	His	Ala	Met	Pro	Gly	Phe	Ile	Trp	Leu	
65					70				75					80		
atc	cgg	agc	ctg	tac	gag	atg	cag	gag	gag	cag	ttg	gcc	cag	gag	gct	288
Ile	Arg	Ser	Leu	Tyr	Glu	Met	Gln	Glu	Glu	Gln	Leu	Ala	Gln	Glu	Ala	
			85					90					95			
gtc	cgt	cgc	ttg	gac	atc	ggg	cac	ctg	aag	ttg	aca	ttt	tgc	aga	gtg	336
Val	Arg	Arg	Leu	Asp	Ile	Gly	His	Leu	Lys	Leu	Thr	Phe	Cys	Arg	Val	
			100					105					110			
ggc	cct	gca	gag	tgt	gct	gcg	ctg	gcc	ttt	gta	ctg	caa	cat	ctc	cag	384
Gly	Pro	Ala	Glu	Cys	Ala	Ala	Leu	Ala	Phe	Val	Leu	Gln	His	Leu	Gln	
		115					120					125				
cgg	cct	gtg	gcc	cta	cag	ctg	gat	tac	aac	tct	gt					419
Arg	Pro	Val	Ala	Leu	Gln	Leu	Asp	Tyr	Asn	Ser						
	130					135										

<210> 193  
 <211> 139  
 <212> PRT  
 <213> Mus musculus

<400> 193

Leu	Gln	Lys	Ala	Glu	Pro	His	Asn	Leu	Gln	Ile	Thr	Ala	Ala	Phe	Leu	
1				5					10					15		
Ala	Gly	Leu	Leu	Ser	Gln	Gln	His	Arg	Asp	Leu	Leu	Ala	Ala	Cys	Gln	
		20						25					30			
Ile	Ser	Glu	Arg	Val	Leu	Leu	Gln	Arg	Gln	Ala	Arg	Ala	Arg	Ser	Cys	
		35					40					45				
Leu	Ala	His	Ser	Leu	Arg	Glu	His	Phe	His	Ser	Ile	Pro	Pro	Ala	Val	
	50					55				60						
Pro	Gly	Glu	Thr	Lys	Ser	Met	His	Ala	Met	Pro	Gly	Phe	Ile	Trp	Leu	
65					70				75					80		
Ile	Arg	Ser	Leu	Tyr	Glu	Met	Gln	Glu	Glu	Gln	Leu	Ala	Gln	Glu	Ala	

				85					90					95					
Val	Arg	Arg	Leu	Asp	Ile	Gly	His	Leu	Lys	Leu	Thr	Phe	Cys	Arg	Val				
			100						105				110						
Gly	Pro	Ala	Glu	Cys	Ala	Ala	Leu	Ala	Phe	Val	Leu	Gln	His	Leu	Gln				
		115					120					125							
Arg	Pro	Val	Ala	Leu	Gln	Leu	Asp	Tyr	Asn	Ser									
	130					135													

<210> 194  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 194  
 ctgcagaagg ctgagccaca caacct 26

<210> 195  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 195  
 acagagttgt aatccagctg tagggccaca 30

<210> 196  
 <211> 3042  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(3042)

<400> 196  
 atg tgc tcg cag gag gct ttt cag gca cag agg agc cag ctg gtc gag 48  
 Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu  
 1 5 10 15

ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg gac tgg 96  
 Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp  
 20 25 30

ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc ttc cac 144  
 Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His  
 35 40 45



ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg gac acc	192
Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr	
50 55 60	
gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc atc gcg gct gcc	240
Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala Ala Ala	
65 70 75 80	
caa gaa gcc cag gcc gac agc cag tcc ccc aag ctg cat ggc tgc tgg	288
Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly Cys Trp	
85 90 95	
gac ccc cac tcg ctc cac cca gcc cga gac ctg cag agt cac cgg cca	336
Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His Arg Pro	
100 105 110	
gcc att gtc agg agg ctc cac agc cat gtg gag aac atg ctg gac ctg	384
Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu Asp Leu	
115 120 125	
gca tgg gag cgg ggt ttc gtc agc cag tat gaa tgt gat gaa atc agg	432
Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg	
130 135 140	
ttg ccg atc ttc aca ccg tcc cag agg gca aga agg ctg ctt gat ctt	480
Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu	
145 150 155 160	
gcc acg gtg aaa gcg aat gga ttg gct gcc ttc ctt cta caa cat gtt	528
Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln His Val	
165 170 175	
cag gaa tta cca gtc cca ttg gcc ctg cct ttg gaa gct gcc aca tgc	576
Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala Thr Cys	
180 185 190	
aag aag tat atg gcc aag ctg agg acc acg gtg tct gct cag tct cgc	624
Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln Ser Arg	
195 200 205	
ttc ctc agt acc tat gat gga gca gag acg ctc tgc ctg gag gac ata	672
Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu Asp Ile	
210 215 220	
tac aca gag aat gtc ctg gag gtc tgg gca gat gtg ggc atg gct gga	720
Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met Ala Gly	
225 230 235 240	
ccc ccg cag aag agc cca gcc acc ctg ggc ctg gag gag ctc ttc agc	768
Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu Phe Ser	
245 250 255	
acc cct ggc cac ctc aat gac gat gcg gac act gtg ctg gtg gtg ggt	816

Thr	Pro	Gly	His	Leu	Asn	Asp	Asp	Ala	Asp	Thr	Val	Leu	Val	Val	Gly		
			260					265					270				
gag	gcg	ggc	agt	ggc	aag	agc	acg	ctc	ctg	cag	cgg	ctg	cac	ttg	ctg		864
Glu	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Gln	Arg	Leu	His	Leu	Leu		
		275					280					285					
tgg	gct	gca	ggg	caa	gac	ttc	cag	gaa	ttt	ctc	ttt	gtc	ttc	cca	ttc		912
Trp	Ala	Ala	Gly	Gln	Asp	Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe	Pro	Phe		
		290				295					300						
agc	tgc	cgg	cag	ctg	cag	tgc	atg	gcc	aaa	cca	ctc	tct	gtg	cgg	act		960
Ser	Cys	Arg	Gln	Leu	Gln	Cys	Met	Ala	Lys	Pro	Leu	Ser	Val	Arg	Thr		
305					310					315					320		
cta	ctc	ttt	gag	cac	tgc	tgt	tgg	cct	gat	gtt	ggc	caa	gaa	gac	atc		1008
Leu	Leu	Phe	Glu	His	Cys	Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu	Asp	Ile		
				325					330					335			
ttc	cag	tta	ctc	ctt	gac	cac	cct	gac	cgt	gtc	ctg	tta	acc	ttt	gat		1056
Phe	Gln	Leu	Leu	Leu	Asp	His	Pro	Asp	Arg	Val	Leu	Leu	Thr	Phe	Asp		
			340					345					350				
ggc	ttt	gac	gag	ttc	aag	ttc	agg	ttc	acg	gat	cgt	gaa	cgc	cac	tgc		1104
Gly	Phe	Asp	Glu	Phe	Lys	Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg	His	Cys		
		355					360					365					
tcc	ccg	acc	gac	ccc	acc	tct	gtc	cag	acc	ctg	ctc	ttc	aac	ctt	ctg		1152
Ser	Pro	Thr	Asp	Pro	Thr	Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn	Leu	Leu		
		370				375					380						
cag	ggc	aac	ctg	ctg	aag	aat	gcc	cgc	aag	gtg	gtg	acc	agc	cgt	ccg		1200
Gln	Gly	Asn	Leu	Leu	Lys	Asn	Ala	Arg	Lys	Val	Val	Thr	Ser	Arg	Pro		
385					390					395					400		
gcc	gct	gtg	tcg	gcg	ttc	ctc	agg	aag	tac	atc	cgc	acc	gag	ttc	aac		1248
Ala	Ala	Val	Ser	Ala	Phe	Leu	Arg	Lys	Tyr	Ile	Arg	Thr	Glu	Phe	Asn		
				405				410						415			
ctc	aag	ggc	ttc	tct	gaa	cag	ggc	atc	gag	ctg	tac	ctg	agg	aag	cgc		1296
Leu	Lys	Gly	Phe	Ser	Glu	Gln	Gly	Ile	Glu	Leu	Tyr	Leu	Arg	Lys	Arg		
			420				425					430					
cat	cat	gag	ccc	ggg	gtg	gcg	gac	cgc	ctc	atc	cgc	ctg	ctc	caa	gag		1344
His	His	Glu	Pro	Gly	Val	Ala	Asp	Arg	Leu	Ile	Arg	Leu	Leu	Gln	Glu		
		435					440					445					
acc	tca	gcc	ctg	cac	ggc	ttg	tgc	cac	ctg	cct	gtc	ttc	tca	tgg	atg		1392
Thr	Ser	Ala	Leu	His	Gly	Leu	Cys	His	Leu	Pro	Val	Phe	Ser	Trp	Met		
		450				455					460						
gtg	tcc	aaa	tgc	cac	cag	gaa	ctg	ttg	ctg	cag	gag	ggg	ggg	tcc	cca		1440
Val	Ser	Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly	Ser	Pro		

465	470	475	480	
aag acc act aca gat atg tac ctg ctg att ctg cag cat ttt ctg ctg				1488
Lys Thr Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe Leu Leu				
	485	490	495	
cat gcc acc ccc cca gac tca gct tcc caa ggt ctg gga ccc agt ctt				1536
His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu				
	500	505	510	
ctt cgg ggc cgc ctc ccc acc ctc ctg cac ctg ggc aga ctg gct ctg				1584
Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu Ala Leu				
	515	520	525	
tgg ggc ctg ggc atg tgc tgc tac gtg ttc tca gcc cag cag ctc cag				1632
Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln				
	530	535	540	
gca gca cag gtc agc cct gat gac att tct ctt ggc ttc ctg gtg cgt				1680
Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu Val Arg				
	545	550	555	560
gcc aaa ggt gtc gtg cca ggg agt acg gcg ccc ctg gaa ttc ctt cac				1728
Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe Leu His				
	565	570	575	
atc act ttc cag tgc ttc ttt gcc gcg ttc tac ctg gca ctc agt gct				1776
Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu Ser Ala				
	580	585	590	
gat gtg cca cca gct ttg ctc aga cac ctc ttc aat tgt ggc agg cca				1824
Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly Arg Pro				
	595	600	605	
ggc aac tca cca atg gcc agg ctc ctg ccc acg atg tgc atc cag gcc				1872
Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile Gln Ala				
	610	615	620	
tcg gag gga aag gac agc agc gtg gca gct ttg ctg cag aag gcc gag				1920
Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys Ala Glu				
	625	630	635	640
ccg cac aac ctt cag atc aca gca gcc ttc ctg gca ggg ctg ttg tcc				1968
Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu Leu Ser				
	645	650	655	
cgg gag cac tgg ggc ctg ctg gct gag tgc cag aca tct gag aag gcc				2016
Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu Lys Ala				
	660	665	670	
ctg ctc cgg cgc cag gcc tgt gcc cgc tgg tgt ctg gcc cgc agc ctc				2064
Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg Ser Leu				
	675	680	685	

cgc aag cac ttc cac tcc atc ccg cca gct gca ccg ggt gag gcc aag	2112
Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu Ala Lys	
690 695 700	
agc gtg cat gcc atg ccc ggg ttc atc tgg ctc atc cgg agc ctg tac	2160
Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser Leu Tyr	
705 710 715 720	
gag atg cag gag gag cgg ctg gct cgg aag gct gca cgt ggc ctg aat	2208
Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly Leu Asn	
725 730 735	
gtt ggg cac ctc aag ttg aca ttt tgc agt gtg ggc ccc act gag tgt	2256
Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr Glu Cys	
740 745 750	
gct gcc ctg gcc ttt gtg ctg cag cac ctc cgg cgg ccc gtg gcc ctg	2304
Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val Ala Leu	
755 760 765	
cag ctg gac tac aac tct gtg ggt gac att ggc gtg gag cag ctg ctg	2352
Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln Leu Leu	
770 775 780	
cct tgc ctt ggt gtc tgc aag gct ctg tat ttg cgc gat aac aat atc	2400
Pro Cys Leu Gly Val Cys Lys Ala Leu Tyr Leu Arg Asp Asn Asn Ile	
785 790 795 800	
tca gac cga ggc atc tgc aag ctc att gaa tgt gct ctt cac tgc gag	2448
Ser Asp Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His Cys Glu	
805 810 815	
caa ttg cag aag tta gct cta ttc aac aac aaa ttg act gac ggc tgt	2496
Gln Leu Gln Lys Leu Ala Leu Phe Asn Asn Lys Leu Thr Asp Gly Cys	
820 825 830	
gca cac tcc atg gct aag ctc ctt gca tgc agg cag aac ttc ttg gca	2544
Ala His Ser Met Ala Lys Leu Leu Ala Cys Arg Gln Asn Phe Leu Ala	
835 840 845	
ttg agg ctg ggg aat aac tac atc act gcc gcg gga gcc caa gtg ctg	2592
Leu Arg Leu Gly Asn Asn Tyr Ile Thr Ala Ala Gly Ala Gln Val Leu	
850 855 860	
gcc gag ggg ctc cga ggc aac acc tcc ttg cag ttc ctg gga ttc tgg	2640
Ala Glu Gly Leu Arg Gly Asn Thr Ser Leu Gln Phe Leu Gly Phe Trp	
865 870 875 880	
ggc aac aga gtg ggt gac gag ggg gcc cag gcc ctg gct gaa gcc ttg	2688
Gly Asn Arg Val Gly Asp Glu Gly Ala Gln Ala Leu Ala Glu Ala Leu	
885 890 895	

ggt gat cac cag agc ttg agg tgg ctc agc ctg gtg ggg aac aac att	2736
Gly Asp His Gln Ser Leu Arg Trp Leu Ser Leu Val Gly Asn Asn Ile	
900 905 910	
ggc agt gtg ggt gcc caa gcc ttg gca ctg atg ctg gca aag aac gtc	2784
Gly Ser Val Gly Ala Gln Ala Leu Ala Leu Met Leu Ala Lys Asn Val	
915 920 925	
atg cta gaa gaa ctc tgc ctg gag gag aac cat ctc cag gat gaa ggt	2832
Met Leu Glu Glu Leu Cys Leu Glu Glu Asn His Leu Gln Asp Glu Gly	
930 935 940	
gta tgt tct ctc gca gaa gga ctg aag aaa aat tca agt ttg aaa atc	2880
Val Cys Ser Leu Ala Glu Gly Leu Lys Lys Asn Ser Ser Leu Lys Ile	
945 950 955 960	
ctg aag ttg tcc aat aac tgc atc acc tac cta ggg gca gaa gcc ctc	2928
Leu Lys Leu Ser Asn Asn Cys Ile Thr Tyr Leu Gly Ala Glu Ala Leu	
965 970 975	
ctg cag gcc ctt gaa agg aat gac acc atc ctg gaa gtc tgg ctc cga	2976
Leu Gln Ala Leu Glu Arg Asn Asp Thr Ile Leu Glu Val Trp Leu Arg	
980 985 990	
ggg aac act ttc tct cta gag gag gtt gac aag ctc ggc tgc agg gac	3024
Gly Asn Thr Phe Ser Leu Glu Glu Val Asp Lys Leu Gly Cys Arg Asp	
995 1000 1005	
acc aga ctc ttg ctt tga	3042
Thr Arg Leu Leu Leu *	
1010	

<210> 197  
 <211> 1013  
 <212> PRT  
 <213> Homo sapiens

<400> 197

Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu	
1 5 10 15	
Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp	
20 25 30	
Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His	
35 40 45	
Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr	
50 55 60	
Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala Ala Ala	
65 70 75 80	
Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly Cys Trp	
85 90 95	
Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His Arg Pro	
100 105 110	

Ala	Ile	Val	Arg	Arg	Leu	His	Ser	His	Val	Glu	Asn	Met	Leu	Asp	Leu	115	120	125
Ala	Trp	Glu	Arg	Gly	Phe	Val	Ser	Gln	Tyr	Glu	Cys	Asp	Glu	Ile	Arg	130	135	140
Leu	Pro	Ile	Phe	Thr	Pro	Ser	Gln	Arg	Ala	Arg	Arg	Leu	Leu	Asp	Leu	145	150	155
Ala	Thr	Val	Lys	Ala	Asn	Gly	Leu	Ala	Ala	Phe	Leu	Leu	Gln	His	Val	165	170	175
Gln	Glu	Leu	Pro	Val	Pro	Leu	Ala	Leu	Pro	Leu	Glu	Ala	Ala	Thr	Cys	180	185	190
Lys	Lys	Tyr	Met	Ala	Lys	Leu	Arg	Thr	Thr	Val	Ser	Ala	Gln	Ser	Arg	195	200	205
Phe	Leu	Ser	Thr	Tyr	Asp	Gly	Ala	Glu	Thr	Leu	Cys	Leu	Glu	Asp	Ile	210	215	220
Tyr	Thr	Glu	Asn	Val	Leu	Glu	Val	Trp	Ala	Asp	Val	Gly	Met	Ala	Gly	225	230	235
Pro	Pro	Gln	Lys	Ser	Pro	Ala	Thr	Leu	Gly	Leu	Glu	Glu	Leu	Phe	Ser	245	250	255
Thr	Pro	Gly	His	Leu	Asn	Asp	Asp	Ala	Asp	Thr	Val	Leu	Val	Val	Gly	260	265	270
Glu	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Gln	Arg	Leu	His	Leu	Leu	275	280	285
Trp	Ala	Ala	Gly	Gln	Asp	Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe	Pro	Phe	290	295	300
Ser	Cys	Arg	Gln	Leu	Gln	Cys	Met	Ala	Lys	Pro	Leu	Ser	Val	Arg	Thr	305	310	315
Leu	Leu	Phe	Glu	His	Cys	Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu	Asp	Ile	325	330	335
Phe	Gln	Leu	Leu	Leu	Asp	His	Pro	Asp	Arg	Val	Leu	Leu	Thr	Phe	Asp	340	345	350
Gly	Phe	Asp	Glu	Phe	Lys	Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg	His	Cys	355	360	365
Ser	Pro	Thr	Asp	Pro	Thr	Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn	Leu	Leu	370	375	380
Gln	Gly	Asn	Leu	Leu	Lys	Asn	Ala	Arg	Lys	Val	Val	Thr	Ser	Arg	Pro	385	390	395
Ala	Ala	Val	Ser	Ala	Phe	Leu	Arg	Lys	Tyr	Ile	Arg	Thr	Glu	Phe	Asn	405	410	415
Leu	Lys	Gly	Phe	Ser	Glu	Gln	Gly	Ile	Glu	Leu	Tyr	Leu	Arg	Lys	Arg	420	425	430
His	His	Glu	Pro	Gly	Val	Ala	Asp	Arg	Leu	Ile	Arg	Leu	Leu	Gln	Glu	435	440	445
Thr	Ser	Ala	Leu	His	Gly	Leu	Cys	His	Leu	Pro	Val	Phe	Ser	Trp	Met	450	455	460
Val	Ser	Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly	Ser	Pro	465	470	475
Lys	Thr	Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe	Leu	Leu	485	490	495
His	Ala	Thr	Pro	Pro	Asp	Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro	Ser	Leu	500	505	510
Leu	Arg	Gly	Arg	Leu	Pro	Thr	Leu	Leu	His	Leu	Gly	Arg	Leu	Ala	Leu	515	520	525
Trp	Gly	Leu	Gly	Met	Cys	Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln	Leu	Gln			

530	535	540
Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu Val Arg		
545	550	555
Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe Leu His		560
	565	570
Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu Ser Ala		575
	580	585
Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly Arg Pro		590
	595	600
Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile Gln Ala		605
	610	615
Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys Ala Glu		620
625	630	635
Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu Leu Ser		640
	645	650
Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu Lys Ala		655
	660	665
Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg Ser Leu		670
	675	680
Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu Ala Lys		685
	690	695
Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser Leu Tyr		700
705	710	715
Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly Leu Asn		720
	725	730
Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr Glu Cys		735
	740	745
Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val Ala Leu		750
	755	760
Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln Leu Leu		765
	770	775
Pro Cys Leu Gly Val Cys Lys Ala Leu Tyr Leu Arg Asp Asn Asn Ile		780
785	790	795
Ser Asp Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His Cys Glu		800
	805	810
Gln Leu Gln Lys Leu Ala Leu Phe Asn Asn Lys Leu Thr Asp Gly Cys		815
	820	825
Ala His Ser Met Ala Lys Leu Leu Ala Cys Arg Gln Asn Phe Leu Ala		830
	835	840
Leu Arg Leu Gly Asn Asn Tyr Ile Thr Ala Ala Gly Ala Gln Val Leu		845
	850	855
Ala Glu Gly Leu Arg Gly Asn Thr Ser Leu Gln Phe Leu Gly Phe Trp		860
865	870	875
Gly Asn Arg Val Gly Asp Glu Gly Ala Gln Ala Leu Ala Glu Ala Leu		880
	885	890
Gly Asp His Gln Ser Leu Arg Trp Leu Ser Leu Val Gly Asn Asn Ile		895
	900	905
Gly Ser Val Gly Ala Gln Ala Leu Ala Leu Met Leu Ala Lys Asn Val		910
	915	920
Met Leu Glu Glu Leu Cys Leu Glu Glu Asn His Leu Gln Asp Glu Gly		925
	930	935
Val Cys Ser Leu Ala Glu Gly Leu Lys Lys Asn Ser Ser Leu Lys Ile		940
945	950	955
		960

Leu Lys Leu Ser Asn Asn Cys Ile Thr Tyr Leu Gly Ala Glu Ala Leu  
                            965                            970                            975  
Leu Gln Ala Leu Glu Arg Asn Asp Thr Ile Leu Glu Val Trp Leu Arg  
                            980                            985                            990  
Gly Asn Thr Phe Ser Leu Glu Glu Val Asp Lys Leu Gly Cys Arg Asp  
                            995                            1000                            1005  
Thr Arg Leu Leu Leu  
                            1010

<210> 198  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic oligonucleotide

<400> 198  
caagatcaag cagccttctt gccctctgg

29

<210> 199  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic oligonucleotide

<400> 199  
catccaggcc tcggagggaa aggacagcag

30

<210> 200  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic oligonucleotide

<400> 200  
cggaattcat gtgctcgag gaggcctttc

30

<210> 201  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic oligonucleotide

<400> 201  
caagttcagc cttaggcagg ac

22



<210> 202  
<211> 324  
<212> DNA  
<213> Homo sapiens

<400> 202  
acgcggggtt ctccacatgg ctgtggagcc tctagaacca tggccaactc gggttctgct 60  
ggggctgact tgccctggcc ttccctgacc accctgcac tggcttctgg agaagtcccg 120  
cactgacctt gttctcccc ccaggttggtg aaatgtgctc gcaggagggt tttcaggcac 180  
agaggagcca gctgggtcgag ctgctggtct cagggtccct ggaaggcttc gagagtgtcc 240  
tggaactggc gctgtcctgg gaggtcctct cctgggagga ctacgagggc ttccacctcc 300  
tgggccagcc tctctccac ttgg 324

<210> 203  
<211> 81  
<212> DNA  
<213> Homo sapiens

<400> 203  
atgggggaag aggggtggttc agcctctcac gatgaggagg aaagagcaag tgcctcctc 60  
ggacattctc cgggttgtga a 81